

PCT

WORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁵ : C12N 9/62		A1	(11) International Publication Number: WO 95/02044 (43) International Publication Date: 19 January 1995 (19.01.95)
(21) International Application Number: PCT/DK94/00274 (22) International Filing Date: 5 July 1994 (05.07.94)		(81) Designated States: AM, AU, BB, BG, BR, BY, CA, CN, CZ, FI, HU, JP, KE, KP, KR, KZ, LK, LT, LV, MG, MN, MW, NO, NZ, PL, RO, RU, SD, SI, SK, TT, UA, US, UZ, VN, European patent (AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BI, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).	
(30) Priority Data: 0811/93 6 July 1993 (06.07.93) DK		Published <i>With international search report.</i>	
(71) Applicant (for all designated States except US): NOVO NORDISK A/S [DK/DK]; Novo Allé, DK-2880 Bagsværd (DK).			
(72) Inventors; and (75) Inventors/Applicants (for US only): DALBØGE, Henrik [DK/DK]; Parkvej 28, DK-2830 Virum (DK). CHRIST-GAU, Stephan [DK/DK]; Ræveskovsvej 10A, DK-2820 Gentofte (DK). ANDERSEN, Lene, Nonboe [DK/DK]; Lindehøjvej 9, DK-3460 Birkerød (DK). KOFOD, Lene, Venke [DK/DK]; Brorfeldevej 8, DK-4350 Ugerløse (DK). KAUPPINEN, Markus, Sakari [FI/DK]; Egegade 10, 5, DK-2200 Copenhagen N (DK). NIELSEN, Jack, Bech [DK/DK]; Ole Olsens Allé 12, DK-2900 Hellerup (DK). DAMBMANN, Claus [DK/DK]; Høje Gladsaxe 61, 7. tb., DK-2860 Søborg (DK).			
(74) Common Representative: NOVO NORDISK A/S; Corporate Patents, Novo Allé, DK-2880 Bagsværd (DK).			
(54) Title: AN ENZYME WITH PROTEASE ACTIVITY			
(57) Abstract			
<p>A DNA construct comprising a DNA sequence encoding an enzyme exhibiting protease activity, which DNA sequence comprises the DNA sequence shown in SEQ ID No. 1 or 2 or an analogue of any of these sequences being at least 80 % homologous to the DNA sequence shown in SEQ ID No. 1 or 2. The proteases encoded by the DNA sequences have an acid pH optimum.</p>			

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AT	Austria	GB	United Kingdom	MR	Mauritania
AU	Australia	GE	Georgia	MW	Malawi
BB	Barbados	GN	Guinea	NE	Niger
BE	Belgium	GR	Greece	NL	Netherlands
BF	Burkina Faso	HU	Hungary	NO	Norway
BG	Bulgaria	IE	Ireland	NZ	New Zealand
BJ	Benin	IT	Italy	PL	Poland
BR	Brazil	JP	Japan	PT	Portugal
BY	Belarus	KE	Kenya	RO	Romania
CA	Canada	KG	Kyrgyzstan	RU	Russian Federation
CF	Central African Republic	KP	Democratic People's Republic of Korea	SD	Sudan
CG	Congo	KR	Republic of Korea	SE	Sweden
CH	Switzerland	KZ	Kazakhstan	SI	Slovenia
CI	Côte d'Ivoire	L	Liechtenstein	SK	Slovakia
CM	Cameroon	LT	Lithuania	SN	Senegal

NAME		NAME	
NAME	NAME	NAME	NAME
AF	Afghanistan	MG	Republic of Madagascar
AL	Albania	ML	Malta
FI	Finland	MN	Mongolia
FR	France		
GA	Gabon		

AN ENZYME WITH PROTEASE ACTIVITY

FIELD OF INVENTION

5 The present invention relates to a DNA construct encoding an enzyme with protease activity, a method of producing the enzyme, an enzyme with protease activity, and an enzyme preparation containing the enzyme.

10 BACKGROUND OF THE INVENTION

Proteases are enzymes capable of cleaving peptide bonds. Acid proteases (i.e. proteases having an acidic pH optimum) have been found to be produced by a number of different organism including 15 mammals and microbes. For instance, microbial acid proteases have been found to be produced by bacterial strains such as strains of *Bacillus* sp. (JP 01240184), fungal strains, e.g. of *Rhizopus* sp. (EP 72978), *Schytalidium* sp. (JP 48091273), *Sulpholobus* sp. and *Thermoplasma* sp. (WO/90 10072) and 20 *Aspergillus* sp. (JP 50121486, EP 82 395).

JP 3058794 discloses the cloning of a gene encoding an acid protease from *R. niveus* and the recombinant expression thereof. The cloning and expression of a gene from *Cryphonectira parasitica* encoding an aspartic protease is described by Choi et al. (1993). Takahashi et al. (1991), Inoue et al. (1991), and JP 25 407 5586 discloses the cloning of a gene from *Aspergillus niger* encoding an acid proteinase (Protease A).

30 Berka et al. (1990) disclose a gene encoding the aspartic proteinase aspergillopepsin A from *Aspergillus awamori*. The cloning of a gene encoding the aspartic proteinase aspergillopepsin O from *Aspergillus oryzae* is described by Berka et al. (1993). The cloning of a gene encoding the acid protease

Acid proteases are widely used industrially, e.g. in the preparation of food and feed, in the leather industry (e.g. to dehair hides), in the production of protein hydrolysates and in the wine making and brewing industry.

5

There is a need for single-component acid proteases for many different applications, especially in the food and feed industry.

10 SUMMARY OF THE INVENTION

It is an object of the present invention to prepare a single-component protease.

15 Accordingly, in a first aspect the invention relates to a DNA construct comprising a DNA sequence encoding an enzyme exhibiting protease activity, which DNA sequence comprises the DNA sequence shown in SEQ ID No. 1 or an analogous sequence thereof being at least 80% homologous to the DNA sequence shown
20 in SEQ ID No. 1.

In a second aspect the invention relates to a DNA construct comprising a DNA sequence encoding an enzyme exhibiting protease activity, which DNA sequence comprises the DNA sequence shown in
25 SEQ ID No. 2 or an analogous sequence thereof being at least 80% homologous to the DNA sequence shown in SEQ ID No. 2.

The DNA sequence shown in SEQ ID No. 1 encodes an enzyme which in the following disclosure is referred to as Protease I. The
30 enzyme encoded by the DNA sequence shown in SEQ ID No. 2 is referred to as Protease II.

By a database homology search it has been found that the DNA sequence shown in SEQ ID Nos. 1 and 2 are generally novel. The

nucleotides. The highest homology to protease II was found to be 75.5% to the *Aspergillus oryzae* aspergillopepsin O as determined for an overlap of 343 nucleotides.

5 In further aspects the invention relates to an expression vector harbouring a DNA construct of the invention, a cell comprising the DNA construct or expression vector and a method of producing an enzyme exhibiting protease activity which method comprises culturing said cell under conditions permitting the production
10 of the enzyme, and recovering the enzyme from the culture.

In a still further aspect the invention relates to an enzyme exhibiting protease activity, which enzyme is encoded by a DNA construct of the invention as defined above or produced by the
15 method of the invention.

In a further important aspect the invention relates to an enzyme with protease activity, which is active at a pH below 7.0 and in the presence of up to 3% hydrogen peroxide. In the present
20 context, the term "is active" as used about the enzyme is intended to indicate that the enzyme is capable of hydrolysing a substrate under the above-mentioned conditions, e.g. as described in example 5 herein.

25 This enzyme of the invention which is active at a pH below 7.0 and in the presence of up to 3% hydrogen peroxidase and which removes more than 80% of the lysozyme from the lenses under the conditions specified in example 5 is termed the " H_2O_2 -stable protease" in the following disclosure. This enzyme is believed
30 to be generally novel.

Also, the present invention provides an enzyme with protease activity, which enzyme is active at a pH below 7.0 and which is specific towards Phe-Val or Lys-Tyr linkages. The term

Protease I and protease II described herein are preferred examples of an enzyme of the invention. The enzymes have been found to be acid proteases, i.e. proteases which has an acid pH optimum.

5

By the present invention it is possible to provide the protease in a highly purified form, i.e. greater than 75% pure, and more preferably greater than 90% pure as determined by SDS gel electrophoresis as described in the Materials and Methods 10 section herein.

In final aspects the invention relates to an enzyme preparation comprising an enzyme of the invention and the use of the enzyme or enzyme preparation for various purposes in which modification 15 or degradation of protein-containing substances is desirable.

DETAILED DESCRIPTION OF THE INVENTION

The DNA construct, vector and method of the invention

20 In the present context the term "analogue" used to define the DNA construct of the invention is understood to include any DNA sequence which encodes an enzyme with protease activity and which is at least 80% homologous to the DNA sequence shown in SEQ ID No. 1 or 2, respectively. The analogous DNA sequence may 25 be a DNA sequence which hybridizes to the same probe as the DNA coding for the protease enzyme under the following conditions: presoaking in 5xSSC and prehybridizing for 1 h at ~55°C in a solution of 5xSSC, 5xDenhardt's solution, 50 mM sodium phosphate, pH 6.8, and 50 µg of denatured sonicated calf thymus 30 DNA, followed by hybridization in the same solution supplemented with 50 µCi 32-P-dCTP labelled probe for 18 h at ~55°C followed by washing three times in 2xSSC, 0.2% SDS at 55°C for 30 minutes. The analogous DNA sequence is preferably at least 90% homologous to the sequence shown in SEQ ID No. 1 or 2,

organism or may be one prepared on the basis of the DNA sequence shown in SEQ ID No. 1 or 2, such as by introduction of nucleotide substitutions which do not give rise to another amino acid sequence of the protease but which correspond to the codon 5 usage of the host organism into which the DNA construct is introduced or nucleotide substitutions which do give rise to a different amino acid sequence and therefore, possibly, a different protein structure which might give rise to a protease mutant with different properties than the native enzyme. Other 10 examples of possible modifications are insertion of one or more nucleotides into the sequence, addition of one or more nucleotides at either end of the sequence, or deletion of one or more nucleotides at either end or within the sequence.

15 Furthermore, it is preferred that the protease encoded by the analogous DNA sequence is immunologically cross-reactive with an antibody raised against a purified protease encoded by the DNA sequence shown in SEQ ID No. 1 or 2.

20 The nucleotide probe with which the analogue of the DNA sequence shown in SEQ ID No. 1 can hybridize may, e.g. be prepared on the basis of any of the following DNA sequences or any combination thereof:

25 (a) AATTAAGCAT CCTCCATCTT
(b) CAAAGCTCAA TCTCGCTAAC
(c) TCCCGCTCTT CTCTCGATCT
(d) CATCATCCCA ATAACCTCGGA
(e) CAAAATGAAG ACCTCTGCTC
30 (f) TCTTGACCGC TGGCCTGTTG
(g) GCACCGCTGC TATTGCTGCT
(h) CCTCTCACCG CGAACGCGCG
(i) ACGTGCTCGC GCTGCCAAGC
(j) TGGCACCAGC CGCAAGAGCA

(n) GAGGTACTCG TCCAACTGGG
 (o) CCGGCGCCGT GCCAT
 (p) AATTAAGCAT CCTCCATCTT CAAAGCTCAA TCTCGCTAAC TCCCCGCTCTT
 CTCTCGATCT CATCATCCCA ATAACCTCGGA CAAAATGAAAG ACCTCTGCTC
 5 TCTTGACCGC TGGCCTGTTG GCACCGCTGC TATTGCTGCT CCTCTCACCG
 CGAACGCCGC ACCTGCTCCG GCTGCCAAGC TGGCACCAAGC CGCAAGAGCA
 AGGGGGGTCT CAAGCCCGGC ACCCAGCGAG GCCATAACCT GACCGGCTCC
 AAGAACACCG GAGGTACTCG TCCAACTGGG CCGGCGCCGT GCCAT

10 These sequences constitute partial sequences of the DNA sequence shown in SEQ ID No. 1 or analogues of such sequences.

The nucleotide probe with which the analogue of the DNA sequence shown in SEQ ID No. 2 can hybridize may, e.g., be prepared on
 15 the basis of any of the following DNA sequences or any combination thereof:

(p1) CTGCTTCTCC TTCTCTTCCT
 (q) CCTCGTGATA TCTGCTTGAA
 20 (r) CATCTCCTCA TCATGGTCGT
 (s) CCTCAACAAG GTGCAGCCTT
 (t) CTTCTGGGTC TGACCAACCGC
 (u) CGCCACTGGT CCCCTGGCCG
 (v) AGCCGCAGGC TTCTGTCCGG
 25 (w) TCAAGAACTT CTCCGTCAAG
 (x) CAGGTCGAGA AGGCAGGCAG
 (y) CAAGGGACGT ACCGTTAAC
 (z) TGCCGGGTCT GTATGCGAAT
 (aa) GCGCTGGCCA AGTATGGCGC
 30 (bb) CCAGGTGCGG CCAGCGTCAA
 (cc) GGCCGCCGCC GTCAGTGGCA
 (dd) GCGTCGTGAC CACCCGCAGG CCAACGACG
 (ee) CTGCTTCTCC TTCTCTTCCT CCTCGTGATA TCTGCTTGAA CATCTCCTCA
 TCATGGTCGT CCTCAACAAG GTGCAGCCTT CTTCTGGGTC TGACCAACCGC

CCAGCGTCAA GGCCGCCGCC GTCAGTGGCA GCGTCGTGAC CACCCGCAGG CCAACGACG

These sequences constitute partial sequences of the DNA sequence shown in SEQ ID No. 2 or analogues of such sequences.

5

A DNA sequence of the invention may be isolated by a general method involving

- 10 - cloning, in suitable vectors, a DNA library from *Aspergillus aculeatus*,
- transforming suitable yeast host cells with said vectors,
- culturing the host cells under suitable conditions to express any enzyme of interest encoded by a clone in the DNA library, and
- 15 - screening for positive clones by determining any protease activity of the enzyme produced by such clones.

20 A more detailed description of this screening method is given in Example 1 below and in WO 93/11249, the contents of which is hereby incorporated by reference.

25 The DNA sequence coding for the enzyme may for instance be isolated by screening a cDNA library of *Aspergillus aculeatus*, e.g. strain CBS 101.43, publicly available from the Centraalbureau voor Schimmelcultures, Delft, NL, and selecting for clones expressing the appropriate enzyme activity (i.e. protease activity as defined by the ability of the enzyme to hydrolyse peptide bonds in proteins and peptides). The appropriate DNA sequence may then be isolated from the clone by 30 standard procedures, e.g. as described in Example 1.

It is expected that a DNA sequence coding for a homologous enzyme, i.e. an analogous DNA sequence, may be derived by similarly screening a cDNA library of another microorganism, in

harzianum, or *T. reesie*, a strain of a *Fusarium* sp., in particular a strain of *F. oxysporum*, a strain of *Rhizopus* sp., e.g. *R. niveus*, a strain of *Schytalidium* sp., or a strain of a *Humicola* sp.

5

Alternatively, the DNA sequence of the invention may, in accordance with well-known procedures, conveniently be isolated from DNA from an appropriate organism by use of synthetic oligonucleotide probes prepared on the basis of a DNA sequence 10 disclosed herein. For instance, a suitable oligonucleotide probe may be prepared on the basis of any of the partial nucleotide sequences shown above.

15 The DNA sequence may subsequently be inserted into a recombinant expression vector. This may be any vector which may conveniently be subjected to recombinant DNA procedures, and the choice of vector will often depend on the host cell into which it is to be introduced. Thus, the vector may be an autonomously replicating 20 vector, i.e. a vector which exists as an extrachromosomal entity, the replication of which is independent of chromosomal replication, e.g. a plasmid. Alternatively, the vector may be one which, when introduced into a host cell, is integrated into the host cell genome and replicated together with the chromosome(s) into which it has been integrated.

25

In the vector, the DNA sequence encoding the protease should be operably connected to a suitable promoter and terminator sequence. The promoter may be any DNA sequence which shows transcriptional activity in the host cell of choice and may be 30 derived from genes encoding proteins either homologous or heterologous to the host cell. The procedures used to ligate the DNA sequences coding for the protease, the promoter and the terminator, respectively, and to insert them into suitable vectors are well known to persons skilled in the art (cf., for 35 instance, U.S. Pat. No. 4,469,459).

The host cell which is transformed with the DNA sequence encoding the enzyme of the invention is preferably a eukaryotic cell, in particular a fungal cell such as a yeast or filamentous fungal cell. In particular, the cell may belong to a species of 5 *Aspergillus*, most preferably *Aspergillus oryzae* or *Aspergillus niger*. Fungal cells may be transformed by a process involving protoplast formation and transformation of the protoplasts followed by regeneration of the cell wall in a manner known per se. The use of *Aspergillus oryzae* as a host microorganism is 10 described in EP 238 023 (of Novo Nordisk A/S), the contents of which are hereby incorporated by reference. The host cell may also be a yeast cell, e.g. a strain of *Saccharomyces*, in particular *Saccharomyces cerevisiae*, *Saccharomyces kluyveri* or *Saccharomyces uvarum*, a strain of *Schizosaccharomyces* sp., such 15 as *Schizosaccharomyces pombe*, a strain of *Hansenula* sp., *Pichia* sp., *Yarrowia* sp. such as *Yarrowia lipolytica*, or *Kluyveromyces* sp. such as *Kluyveromyces lactis*.

In a still further aspect, the present invention relates to a 20 method of producing an enzyme with protease activity, wherein a suitable host cell transformed with a DNA construct of the invention encoding the enzyme is cultured under conditions permitting the production of the enzyme, and the resulting enzyme is recovered from the culture.

25 The medium used to culture the transformed host cells may be any conventional medium suitable for growing the host cells in question. The expressed protease may conveniently be secreted into the culture medium and may be recovered therefrom by well-known procedures including separating the cells from the medium by centrifugation or filtration, precipitating proteinaceous components of the medium by means of a salt such as ammonium sulphate, followed by chromatographic procedures such as ion exchange chromatography, affinity chromatography, or the like.

10

Preferably, the protease of the invention (e.g. the H₂O₂-stable or the Lys-Tyr or Phe-Val specific protease) is active at a pH in the range of 2-7, such as at a pH below 6.0, e.g. in the range of 2-6, and most preferably in the pH range of 4-6.

5

It will be understood that both acidic proteases are active in the presence of 0.01-5% hydrogen peroxide, such as 0.1-5%, 0.5-4%, 1-4% or 2-3% hydrogen peroxide and are applicable to contact lens cleaning.

10

A preferred example of an H₂O₂-stable protease of the invention is the enzyme encoded by the DNA sequence shown in SEQ ID No. 1 or an analogue thereof as defined above, which is at least 80% homologous to said DNA sequence.

15

A preferred example of the Lys-Tyr or Phe-Val specific protease of the invention is the enzyme encoded by the DNA sequence shown in SEQ ID No. 2 or an analogue thereof as defined above, which is at least 80% homologous to said DNA sequence.

20

The enzyme of the invention is preferably immunologically reactive with an antibody raised against a purified protease derived from *Aspergillus aculeatus*, CBS 101.43 and being encoding by the DNA sequence shown in SEQ ID No. 1 or 2. In the 25 present context, the term "derived from" is intended not only to indicate a protease produced by strain CBS 101.43, but also a protease encoded by a DNA sequence isolated from strain CBS 101.43 and produced in a host organism transformed with said DNA sequence.

30

While the H₂O₂-stable protease and the Lys-Tyr or Phe-Val specific protease of the invention both were obtained from a strain of the fungal species *Aspergillus aculeatus*, it is contemplated that such enzymes are obtainable from other

a bacterium or a fungus such as a strain of *Aspergillus*, *Rhizopus*, *Trichoderma*, e.g. *T. reesei* or *T. harzianum*, *Penicillium*, *Fusarium*, *Schytalidium* or *Humicola*, e.g. *H. insolens* or *H. lanuginosa*, or a strain of *Bacillus*.

5

Examples of *Aspergillus* sp. include *A. niger*, *A. oryzae* or *A. aculeatus*, such as *A. aculeatus* CBS 101.43.

In a still further aspect, the present invention relates to an 10 enzyme preparation useful for the degradation or modification of protease containing materials, said preparation being enriched in an enzyme exhibiting protease activity as described above.

The enzyme preparation having been enriched with an enzyme of 15 the invention may e.g. be an enzyme preparation comprising multiple enzymatic activities, in particular an enzyme preparation comprising multiple plant cell wall degrading enzymes such as Pectinex®, Pectinex Ultra SP®, Gamanase, Celluclast or Celluzyme or protease and/or exopeptidase-containing enzyme 20 preparations such as Neutraser®, Alcalase® or Flavourzyme® (all available from Novo Nordisk A/S). In the present context, the term "enriched" is intended to indicate that the protease activity of the enzyme preparation has been increased, e.g. with an enrichment factor of at least 1.1, conveniently due to 25 addition of an enzyme of the invention prepared by the method described above.

Alternatively, the enzyme preparation enriched in an enzyme exhibiting protease activity may be one which comprises an 30 enzyme of the invention as the major enzymatic component, e.g. a mono-component enzyme preparation.

The enzyme preparation may be prepared in accordance with methods known in the art and may be in the form of a liquid or

methods known in the art.

The enzyme preparation according to the invention may be used as an agent for degradation or modification of plant cell walls.

5 Some proteins, like extensins, are components of plant cell walls. Proteases will therefore facilitate the degradation or modification of plant cell walls. Such a protease containing plant cell wall degrading enzyme preparation can be used for many different applications like extraction of oil from plant

10 sources like olives and rape or for production of juice from different fruits like apples, pears and citrus.

The enzyme preparation may additionally contain one or more other plant cell wall degrading enzymes such as a pectin lyase,

15 pectate lyase, endoglucanase, arabinanase, xylanase, glucanase, galactanase, mannanase, α -galactosidase, rhamnogalacturonase, pectin acetyl esterase, polygalacturonase, protease, exo-peptidase or pectin methylesterase. The preparation may further contain one or more enzymes exhibiting exo-activity on the same

20 substrates as the above-mentioned endo-enzymes. The proteases according to the invention work at the same pH and temperature conditions as many other cell wall degrading enzymes, and are thereby particular well suited for such applications.

25 The additional enzyme(s) may be producible by means of a microorganism belonging to the genus *Aspergillus*, preferably *Aspergillus niger*, *Aspergillus aculeatus*, *Aspergillus awamori* or *Aspergillus oryzae*, or *Trichoderma*.

30 The protease enzyme preparation according to the invention may also be used in the wine industry, to prevent haze or to dissolve haze, as proteins often take part in the undesirable haze formation. The proteases according to the invention are active under the conditions present under fermentation and

The enzyme or enzyme preparation of the invention may be used in baking, e.g. in order to weaken the gluten components of flour so as to obtain a softening of so-called hard flour. The use of weak flour is important for the preparation of dough which must 5 be very extensible and not elastic, e.g. in the preparation of extruded baked products, biscuits and other products which must keep their original shape during transport and baking. The proteases of the invention constitute a desirable alternative to conventionally used agents for weakening of flour, such as 10 sodium metabisulphite (SMS). The use of SMS is considered to be undesirable because of potential health risks.

The protease preparation may also be used in the food and feed industry to improve the digestibility of proteins. For instance, 15 the enzyme or enzyme preparation may be added to animal feed or may be used to process animal feed, in particular feed for piglets or poultry. Thereby, the digestibility of components of the feed may be increased resulting in an improved growth rate and efficiency of feed utilisation of the animals, cf. Brenes et 20 al. (1993).

Further the enzyme or enzyme preparation of the invention may be useful to make protein hydrolysates from, e.g., vegetable proteins like soy, pea, lupin or rape seed protein, milk like 25 casein, meat proteins, or fish proteins. The protease may be used for protein hydrolysates to improve the solubility, consistency, taste, or fermentability, to reduce antigenicity or for other purposes to make food, feed or dedical products. The protease may be used alone or together with other proteases or 30 together with other enzymes like exopeptidases. The use of the protease of the invention together with exopeptidase rich enzyme preparations will improve the taste of the protein hydrolysates.

The protease preparation may also be used to modify proteins,

Furthermore, the enzyme or enzyme preparation may be used in the processing of fish or meat, e.g. to change texture and/or viscosity.

5 The protease preparation may also be used to facilitate fermentative processes, like yeast fermentation of barley, malt and other raw materials for the production of e.g. beer.

Furthermore, the enzyme or enzyme preparation of the invention
10 may be useful in the leather industry e.g. to remove hairs from
hides. The low pH optimum of the protease is an advantage as the
subsequent tanning of the hides is carried under acid
conditions. The protease preparation is useful for production of
peptides from proteins, where it is advantages to use a cloned
15 enzyme essentially free from other proteolytic activities.

Further the protease preparation can be used to degrade protein
in order to facilitate purification of or to upgrade different
products, like in purification or upgrading of gums, like guar
20 gum, xanthan gum, degumming of silk, or improvement of the
quality of wool.

Due to the stability towards hydrogen peroxide both proteases of
the invention are of particular use for cleaning of contact
25 lenses and other applications involving the use of hydrogen
peroxide, in which protein-containing material is to be removed.

For the above uses, the dosage of the enzyme preparation of the
invention and other conditions under which the preparation is
30 used may be determined on the basis of methods known in the art.

The invention is further described in the accompanying drawing
in which

28 FIGURE 1

15

Fig. 2 the temperature-activity profiles of Protease I and II, respectively,

5 Fig. 3 and 4 the pH stability of Protease I and II, respectively,

Fig. 5 and 6 the temperature stability of Protease I and II, respectively,

10 Fig. 7 the performance of various proteases in the cleaning of contact lenses, and

Fig. 8 the gluten stretching effect of an enzyme of the invention.

15

The invention is described in further detail in the following examples which are not in any way intended to limit the scope of the invention as claimed.

20 MATERIALS AND METHODS

Donor organism: mRNA was isolated from *Aspergillus aculeatus*, CBS 101.43, grown in a soy-containing fermentation medium with agitation to ensure sufficient aeration. Mycelia were harvested 25 after 3-5 days' growth, immediately frozen in liquid nitrogen and stored at -80°C.

Yeast strains: The *Saccharomyces cerevisiae* strain used was 30 YNG231 (MAT alpha, leu2, ura3-52, his4-539, pep4-delta 1, cir+) or JG169 (MAT α ; ura 3-52; leu 2-3, 112; his 3-D200; pep 4-113; prc1::HIS3; prb1:: LEU2; cir+).

Plasmids: The expression plasmid pYHD17 containing the yeast TPI promoter was prepared from the commercially available plasmid

The Aspergillus expression vector pHD414 is a derivative of the plasmid p775 (described in EP 238 023). The construction of pHD414 is further described in WO 93/11249. pHD414 contains the *A. niger* glucoamylase terminator and the *A. oryzae* TAKA amylase 5 promoter.

Extraction of total RNA: The total RNA was prepared by extraction with guanidinium thiocyanate followed by ultracentrifugation through a 5.7 M CsCl cushion essentially as 10 described by Chirgwin *et al.*, 1979 and in WO 93/11249.

Isolation of poly(A)⁺RNA: The poly(A)⁺ RNAs were isolated by oligo(dT)-cellulose affinity chromatography (Aviv & Leder, 1972). Typically, 0.2 g of oligo(dT) cellulose (Boehringer 15 Mannheim) was preswollen in 10 ml of 1 x column loading buffer (20 mM Tris-Cl, pH 7.6, 0.5 M NaCl, 1 mM EDTA, 0.1 % SDS), loaded onto a DEPC-treated, plugged plastic column (Poly Prep Chromatography Column, Bio Rad), and equilibrated with 20 ml 1 x loading buffer. The total RNA was heated at 65 °C for 8 min., 20 quenched on ice for 5 min, and after addition of 1 vol 2 x column loading buffer to the RNA sample loaded onto the column. The eluate was collected and reloaded 2-3 times by heating the sample as above and quenching on ice prior to each loading. The oligo(dT) column was washed with 10 vols of 1 x loading buffer, 25 then with 3 vols of medium salt buffer (20 mM Tris-Cl, pH 7.6, 0.1 M NaCl, 1 mM EDTA, 0.1 % SDS), followed by elution of the poly(A)⁺ RNA with 3 vols of elution buffer (10 mM Tris-Cl, pH 7.6, 1 mM EDTA, 0.05 % SDS) preheated to + 65 °C, by collecting 500 µl fractions. The OD₂₆₀ was read for each collected fraction, 30 and the mRNA containing fractions were pooled and ethanol precipitated at - 20 °C for 12 h. The poly(A)⁺ RNA was collected by centrifugation, resuspended in DEPC-DIW and stored in 5-10 µg aliquots at - 80 °C.

membranes (Hybond-N, Amersham) with 10 x SSC (Sambrook et al., 1989) as transfer buffer. Three random-primed (Feinberg & Vogelstein, 1983) ³²P-labeled cDNA probes were used in individual hybridizations: 1) a 1.3 kb Not I-Spe I fragment for polygalacturonase I from *A. aculeatus*, 2) a 1.3 kb Not I-Spe I fragment encoding endoglucanase I from *A. aculeatus* and 3) a 1.2 kb Eag I fragment coding for galactanase I from *A. aculeatus*. Northern hybridizations were carried out in 5 x SSC (Sambrook et al., 1989), 5 x Denhardt's solution (Sambrook et al., 1989), 0.5 % SDS (w/v) and 100 µg/ml denatured salmon sperm DNA with a probe concentration of ca. 2 ng/ml for 16 h at 65 °C followed by washes in 5 x SSC at 65 °C (2 x 15 min), 2 x SSC, 0.5 % SDS (1 x 30 min), 0.2 x SSC, 0.5 % SDS (1 X 30 min), and 5 x SSC (2 x 15 min). After autoradiography at - 80 °C for 12 h, the probe #1 was removed from the filter according to the manufacturer's instructions and rehybridized with probe #2, and eventually with probe #3. The RNA ladder from Bethesda Research Laboratories was used as a size marker.

20 cDNA synthesis:

25 **First strand synthesis:** Double-stranded cDNA was synthesized from 5 µg of *A. aculeatus* poly(A)⁺ RNA by the RNase H method (Gubler & Hoffman 1983, Sambrook et al., 1989) using the hairpin modification. The poly(A)⁺RNA (5 µg in 5 µl of DEPC-treated water) was heated at 70 °C for 8 min., quenched on ice, and combined in a final volume of 50 µl with reverse transcriptase buffer (50 mM Tris-Cl, pH 8.3, 75 mM KCl, 3 mM MgCl₂, 10 mM DTT, Bethesda Research Laboratories) containing 1 mM each dNTP (Pharmacia), 40 units of human placental ribonuclease inhibitor (RNasin, Promega), 10 µg of oligo(dT)₁₂₋₁₈ primer (Pharmacia) and 1000 units of SuperScript II RNase H- reverse transcriptase (Bethesda Research Laboratories). First-strand cDNA was synthesized by incubating the reaction mixture at 45 °C for 1 h.

pH 7.5, 1 mM EDTA was added, and the mRNA:cDNA hybrids were ethanol precipitated for 12 h at - 20 °C by addition of 40 µg glycogen carrier (Boehringer Mannheim) 0.2 vols 10 M NH₄Ac and 2.5 vols 96 % EtOH. The hybrids were recovered by 5 centrifugation, washed in 70 % EtOH, air dried and resuspended in 250 µl of second strand buffer (20 mM Tris-Cl, pH 7.4, 90 mM KCl, 4.6 mM MgCl₂, 10 mM (NH₄)₂SO₄, 16 µM BNAD⁺) containing 100 µM each dNTP, 44 units of *E. coli* DNA polymerase I (Amersham), 6.25 units of RNase H (Bethesda Research Laboratories) and 10.5 10 units of *E. coli* DNA ligase (New England Biolabs). Second strand cDNA synthesis was performed by incubating the reaction tube at 16 °C for 3 h, and the reaction was stopped by addition of EDTA to 20 mM final concentration followed by phenol extraction.

15 **Mung bean nuclease treatment:** The double-stranded (ds) cDNA was ethanol precipitated at - 20 °C for 12 h by addition of 2 vols of 96 % EtOH, 0.1 vol 3 M NaAc, pH 5.2, recovered by centrifugation, washed in 70 % EtOH, dried (SpeedVac), and resuspended in 30 µl of Mung bean nuclease buffer (30 mM NaAc, 20 pH 4.6, 300 mM NaCl, 1 mM ZnSO₄, 0.35 mM DTT, 2 % glycerol) containing 36 units of Mung bean nuclease (Bethesda Research Laboratories). The single-stranded hair-pin DNA was clipped by incubating the reaction at 30 °C for 30 min, followed by addition of 70 µl 10 mM Tris-Cl, pH 7.5, 1 mM EDTA, phenol 25 extraction, and ethanol precipitation with 2 vols of 96 % EtOH and 0.1 vol 3M NaAc, pH 5.2 at - 20 °C for 12 h.

Blunt-ending with T4 DNA polymerase: The ds cDNA was blunt-ended with T4 DNA polymerase in 50 µl of T4 DNA polymerase buffer (20 mM Tris-acetate, pH 7.9, 10 mM MgAc, 50 mM KAc, 1 mM DTT) 30 containing 0.5 mM each dNTP and 7.5 units of T4 DNA polymerase (Invitrogen) by incubating the reaction mixture at + 37 °C for 15 min. The reaction was stopped by addition of EDTA to 20 mM final concentration followed by phenol extraction and ethanol

Adapter ligation and size selection: All 1 µl reactions were combined

the cDNA was ligated to non-palindromic BstX I adaptors (1 μ g/ μ l, Invitrogen) in 30 μ l of ligation buffer (50 mM Tris-Cl, pH 7.8, 10 mM MgCl₂, 10 mM DTT, 1 mM ATP, 25 μ g/ml bovine serum albumin) containing 600 pmol BstX I adaptors and 5 units of T4 ligase (Invitrogen) by incubating the reaction mix at + 16 °C for 12 h. The reaction was stopped by heating at + 70 °C for 5 min, and the adapted cDNA was size-fractionated by agarose gel electrophoresis (0.8 % HSB-agarose, FMC) to separate unligated adaptors and small cDNAs. The cDNA was size-selected with a cut-off at 0.7 kb, and the cDNA was electroeluted from the agarose gel in 10 mM Tris-Cl, pH 7.5, 1 mM EDTA for 1 h at 100 volts, phenol extracted and ethanol precipitated at - 20 °C for 12 h as above.

15 **Construction of cDNA libraries:** The adapted, ds cDNA was recovered by centrifugation, washed in 70 % EtOH and resuspended in 25 ml DIW. Prior to large-scale library ligation, four test ligations were carried out in 10 μ l of ligation buffer (same as above) each containing 1 μ l ds cDNA (reaction tubes #1 - #3), 2 units of T4 ligase (Invitrogen) and 50 ng (tube #1), 100 ng (tube #2) and 200 ng (tubes #3 and #4) Bst XI cleaved yeast expression vector either pYES 2.0 vector Invitrogen or yHD17). The ligation reactions were performed by incubation at + 16 °C for 12 h, heated at 70 °C for 5 min, and 1 μ l of each ligation 20 electroporated (200 Ω , 2.5 kV, 25 μ F) to 40 μ l competent *E. coli* 1061 cells (OD₆₀₀ = 0.9 in 1 liter LB-broth, washed twice in cold DIW, once in 20 ml of 10 % glycerol, resuspended in 2 ml 10 % glycerol). After addition of 1 ml SOC to each transformation 25 mix, the cells were grown at + 37 °C for 1 h, 50 μ l plated on LB + ampicillin plates (100 μ g/ml) and grown at + 37 °C for 12h.

Using the optimal conditions a large-scale ligation was set up in 40 μ l of ligation buffer containing 9 units of T4 ligase, and the reaction mix was electroporated to 40 μ l competent *E. coli* 1061 cells (OD₆₀₀ = 0.9 in 1 liter LB-broth, washed twice in cold DIW, once in 20 ml of 10 % glycerol, resuspended in 2 ml 10 % glycerol). After addition of 1 ml SOC to each transformation mix, the cells were grown at + 37 °C for 1 h, 50 μ l plated on LB + ampicillin plates (100 μ g/ml) and grown at + 37 °C for 12h.

After transformation, the cells were harvested and the aliquots were transformed

20

into electrocompetent *E. coli* 1061 cells using the same electroporation conditions as above, and the transformed cells were titered and the library plated on LB + ampicillin plates with 5000-7000 c.f.u./plate. To each plate was added 3 ml of 5 medium. The bacteria were scraped off, 1 ml glycerol was added and stored at -80°C as pools. The remaining 2 ml were used for DNA isolation. If the amount of DNA was insufficient to give the required number of yeast transformants, large scale DNA was prepared from 500 ml medium (TB) inoculated with 50 μ l of -80°C 10 bacterial stock propagated overnight.

Construction of yeast libraries: To ensure that all the bacterial clones were tested in yeast, a number of yeast transformants 5 times larger than the number of bacterial clones 15 in the original pools was set as the limit.

One μ l aliquots of purified plasmid DNA (100 ng/ μ l) from individual pools were electroporated (200 Ω , 1.5 kV, 25 μ F) into 20 μ l competent *S. cerevisiae* JG 169 cells (OD600 = 1.5 in 500 ml YPD, washed twice in cold DIW, once in cold 1 M sorbitol, resuspended in 0.5 ml 1 M sorbitol, Becker & Guarante, 1991). After addition of 1 ml 1M cold sorbitol, 80 μ l aliquots were plated on SC + glucose - uracil to give 250-400 c.f.u./plate and incubated at 30°C for 3 - 5 days.

25

Isolation of a cDNA gene for expression in *Aspergillus*:

One or more of protease-producing colonies were inoculated into 20 ml YNB-1 broth in a 50 ml glass test tube. The tube was shaken for 2 days at 30°C. The cells were harvested by 30 centrifugation for 10 min. at 3000 rpm.

The cells were resuspended in 1 ml 0.9 M sorbitol, 0.1 M EDTA, pH 7.5. The pellet was transferred to an Eppendorf tube, and spun for 30 seconds at full speed. The cells were resuspended in

(spheroplasts) was resuspended in 0.4 ml TE. 90 μ l of (1.5 ml 0.5 M EDTA pH 8.0, 0.6 ml 2 M Tris-Cl pH 8.0, 0.6 ml 10% SDS) was added, and the suspension was incubated at 65°C for 30 minutes. 80 μ l 5 M KOAc was added, and the suspension was 5 incubated on ice for at least 60 minutes and spun for 15 minutes at full speed. The supernatant was transferred to a fresh tube which was filled with EtOH (room temp.) followed by thorough but gentle mixing and spinning for 30 seconds. The pellet was washed with cold 70% EtOH, spun for 30 seconds and dried at room 10 temperature. The pellet was resuspended in 50 μ l TE and spun for 15 minutes. The supernatant was transferred to a fresh tube. 2.5 μ l 10 mg/ml RNase was added, followed by incubation at 37°C for 30 minutes and addition of 500 μ l isopropanol with gentle 15 mixing. The mixture was spun for 30 seconds, and the supernatant was removed. The pellet was rinsed with cold 96% EtOH and dried at room temperature. The DNA was dissolved in 50 μ l water to a final concentration of approximately 100 μ l/ml.

Transformation of *Aspergillus oryzae* or *Aspergillus niger*
20 (general procedure)

100 ml of YPD (Sherman et al., Methods in Yeast Genetics, Cold Spring Harbor Laboratory, 1981) is inoculated with spores of *A. oryzae* or *A. niger* and incubated with shaking at 37°C for about 25 2 days. The mycelium is harvested by filtration through miracloth and washed with 200 ml of 0.6 M MgSO₄. The mycelium is suspended in 15 ml of 1.2 M MgSO₄, 10 mM NaH₂PO₄, pH = 5.8. The suspension is cooled on ice and 1 ml of buffer containing 120 mg 30 of Novozym® 234, batch 1687 is added. After 5 minutes 1 ml of 12 mg/ml BSA (Sigma type H25) is added and incubation with gentle agitation continued for 1.5-2.5 hours at 37°C until a large number of protoplasts is visible in a sample inspected under the microscope.

performed for 15 minutes at 100 g and the protoplasts are collected from the top of the $MgSO_4$ cushion. 2 volumes of STC (1.2 M sorbitol, 10 mM Tris-HCl, pH = 7.5. 10 mM $CaCl_2$) are added to the protoplast suspension and the mixture is 5 centrifugated for 5 minutes at 1000 g. The protoplast pellet is resuspended in 3 ml of STC and repelleted. This is repeated. Finally the protoplasts are resuspended in 0.2-1 ml of STC.

100 μ l of protoplast suspension is mixed with 5-25 μ g of the 10 appropriate DNA in 10 μ l of STC. Protoplasts are mixed with p3SR2 (an *A. nidulans* amds gene carrying plasmid). The mixture is left at room temperature for 25 minutes. 0.2 ml of 60% PEG 4000 (BDH 29576). 10 mM $CaCl_2$ and 10 mM Tris-HCl, pH = 7.5 is added and carefully mixed (twice) and finally 0.85 ml of the 15 same solution is added and carefully mixed. The mixture is left at room temperature for 25 minutes, spun at 2500 g for 15 minutes and the pellet is resuspended in 2 ml of 1.2 M sorbitol. After one more sedimentation the protoplasts are spread on the appropriate plates. Protoplasts are spread on minimal plates 20 (Cove Biochem.Biophys.Acta 113 (1966) 51-56) containing 1.0 M sucrose, pH = 7.0, 10 mM acetamide as nitrogen source and 20 mM CsCl to inhibit background growth. After incubation for 4-7 days at 37°C spores are picked and spread for single colonies. This 25 procedure is repeated and spores of a single colony after the second reisolation is stored as a defined transformant.

30 **Immunological cross-reactivity:** Antibodies to be used in determining immunological cross-reactivity may be prepared by use of a purified protease. More specifically, antiserum against a protease of the invention may be raised by immunizing rabbits (or other rodents) according to the procedure described by N. Axelsen *et al.* in: A Manual of Quantitative Immunoelectrophoresis, Blackwell Scientific Publications, 1973, Chapter 23, or A. Johnstone and R. Thorpe, Immunochemistry in

((NH₄)₂ SO₄), followed by dialysis and ion exchange chromatography, e.g. on DEAE-Sephadex. Immunochemical characterization of proteins may be done either by Ouchterlony double-diffusion analysis (O. Ouchterlony in: Handbook of Experimental Immunology (D.M. Weir, Ed.), Blackwell Scientific Publications, 1967, pp. 655-706), by crossed immunoelectrophoresis (N. Axelsen *et al.*, supra, Chapters 3 and 4), or by rocket immunoelectrophoresis (N. Axelsen *et al.*, Chapter 2).

10

Media:

YPD: 10 g yeast extract, 20 g peptone, H₂O to 810 ml. Autoclaved, 90 ml 20% glucose (sterile filtered) added.

15

10 x Basal salt: 66.8 g yeast nitrogen base, 100 g succinic acid, 60 g NaOH, H₂O ad 1000 ml, sterile filtered.

20

SC-URA: 90 ml 10 x Basal salt, 22.5 ml 20 % casamino acids, 9 ml 1% tryptophan, H₂O ad 806 ml, autoclaved, 3.6 ml 5% threonine and 90 ml 20% glucose or 20% galactose added.

25

SC-H broth: 7.5 g/l yeast nitrogen base without amino acids, 11.3 g/l succinic acid, 6.8 g/l NaOH, 5.6 g/l casamino acids without vitamins, 0.1 g/l tryptophan. Autoclaved for 20 min. at 121°C. After autoclaving, 10 ml of a 30% galactose solution, 5 ml of a 30% glucose solution and 0.4 ml of a 5% threonine solution were added per 100 ml medium.

30

SC-H agar: 7.5 g/l yeast nitrogen base without amino acids, 11.3 g/l succinic acid, 6.8 g/l NaOH, 5.6 g/l casamino acids without vitamins, 0.1 g/l tryptophan, and 20 g/l agar (Bacto). Autoclaved for 20 min. at 121°C. After autoclaving, 55 ml of a 20% galactose solution and 1.8 ml of a 5% threonine solution

TMH-1 agar: 7.5 g/l yeast nitrogen base, 11.3 g/l casamino acids

Autoclaved for 20 min. at 121°C. After autoclaving, 25 ml of a 13.6% yeast nitrogen base without amino acids, 25 ml of a 40% glucose solution, 1.5 ml of a 1% L-leucine solution and 1.5 ml of a 1% histidine solution were added per 450 ml agar.

5

YNB-1 broth: Composition as YNB-1 agar, but without the agar.

FG-4-Agar: 35 g/L agar, 30 g/L Soy bean meal, 15 g/L maltodextrin (Glucidex 6), 5 g/L Bacto pepton, pH 7. Autoclaved 10 40 min at 121°C

FG-4 medium: 30 g/L Soy bean meal, 15 g/L maltodextrin (Glucidex 6), 5 g/L Bacto peptone. Autoclaved 40 min at 121°C.

15 MDU-2 medium: 45 g/L maltose, 1 g/L MgSO₄ - 7 H₂O, 1 g/L NaCl, 2g/L K₂SO₄, 12 g/L KH₂PO₄, 0.1 ml/L Pluronic 61 L, 0.5 ml/L Trace metal solution. pH 5.0. Autoclaved 20 min at 121°C. 15 ml/L 50% sterile filtered urea is added after autoclaving.

20 Casein overlayer gel: 1% agarose, 0.5% casein in a buffer with a pH of 5.5. The gel was boiled and then cooled to 55°C before the overlayer was poured onto agar plates.

Fed batch fermentation

25 The medium used for fed-batch fermentation of protease I or II by *A. oryzae* comprised maltodextrin as a carbon source, urea as a nitrogen source and yeast extract.

30 The fed batch fermentation was performed by innoculating a shake flask culture of the *A. oryzae* host cells in question into a medium comprising 3.5% of the carbon source and 0.5% of the nitrogen source. After 24 hours of cultivation at pH 5.0 and 34°C the continuous supply of additional carbon and nitrogen sources were initiated. The carbon source was kept as the

After which the culture was harvested.

characterization of enzymes

Proteolytic activity

1 hemoglobin protease unit (hpu) is defined as the amount of
5 enzyme liberating 1 millimole of primary amino groups
(determined by comparison with a serine standard) per minute
under standard conditions as described below:

A 2% (w/v) solution of hemoglobin (bovine, supplied by Sigma) is
10 prepared with the Universal Buffer described by Britton and
Robinson, J. Chem. Soc., 1931, p. 1451), adjusted to a pH of
5.5. 2 ml of the substrate solution are pre-incubated in a water
bath for 10 min. at 25°C. 1 ml of an enzyme solution containing
15 b g/ml of the enzyme preparation, corresponding to about 0.2-0.3
hpu/ml of the Universal Buffer (pH 5.5) is added. After 30 min.
of incubation at 25°C, the reaction is terminated by the addition
of a quenching agent (5 ml of a solution containing 17.9 g
15 of trichloroacetic acid, 29.9 g of sodium acetate and 19.8 g of
acetic acid made up to 500 ml with deionized water). A blank is
20 prepared in the same way as the test solution with the exception
that the quenching agent is added prior to the enzyme solution.
The reaction mixtures are kept for 20 min. in a water bath after
which they are filtered through Whatman 42 paper filters.

25 Primary amino groups are determined by their colour development
with o-phthaldialdehyde (OPA), as follows: 7.62 g of disodium
tetraborate decahydrate and 2.0 g of sodium dodecylsulfate are
dissolved in 150 ml of water. 160 mg of OPA dissolved in 4 ml of
30 methanol were then added together with 400 μ l of β -
mercaptoethanol after which the solution is made up to 200 ml
with water. To 3 ml of the OPA reagent are added 400 μ l of the
filtrates obtained above, with mixing. The optical density (OD)
at 340 nm is measured after about 5 min. The OPA test is also
performed on a solution containing 10 μ g of serine in
order to determine the sensitivity of the test.

measurements by means of the following equipment:

26

$$\text{hpu/ml enzyme solution: } \frac{(OD_i - OD_b) \times C_{\text{ser}} \times Q}{(OD_{\text{ser}} - OD_b) \times MW_{\text{ser}} \times t_i}$$

5 hpu/g of enzyme preparation = hpu/ml: b

wherein OD_i , OD_b , OD_{ser} and OD_b is the optical density of the test solution, blank, serine standard and buffer, respectively, C_{ser} is the concentration of serine (mg/ml) in the standard (in this 10 case 0.1 mg/ml), and MW_{ser} is the molecular weight of serine (105.09). Q is the dilution factor for the enzyme solution (in this case 8) and t_i is the incubation time in minutes (in this case 30 minutes).

15 Inhibition

The following inhibitors were tested:

15 Pepstatin (aspartic acid inhibitor) (1mM)
 PMSF (serine protease inhibitor) (0.1%)
 20 PEFABLOC (serine protease inhibitor) (0.1%)
 EDTA (metallopeptidase inhibitor) (0.1M)
 all available from Sigma except for PEFABLOC which is available from Pentapharm, Basel, Switzerland.

25 Residual activity was determined as HPU/l at pH 5.5.

25 pH activity profiles were determined as HPU/l at different pH values (4-8).
 30 pH-stability was determined by letting an enzyme solution (0.3 HPU/l) stand for 30, 60 and 120 minutes, respectively, at 50°C and different pH-values (4-5-6-7-8) and measure proteolytic activity before and after standing.

Temperature stability was determined by letting an enzyme

solution (0.3 HPU/l) stand for 30, 60 and 120 minutes at pH 5 and at different temperatures (25-40-50-60°C), and measure proteolytic activity before and after standing.

5 SDS gel electrophoresis and isoelectric focusing was carried out on the Phast-System from Pharmacia using a Gradient 8-25 and the IEF 3-9, respectively, according to the manufacturers instructions.

10 Specificity

The specificity of proteases of the invention is determined as follows:

0.5 ml of 1 mg/ml human insulin or bovine glucagon in Universal Buffer, pH 5.5 (vide supra), and 75 µl of protease I and II, 15 respectively, (0.6 hpu/l) in the same buffer were incubated for 120 min. at 37°C. The reaction was terminated by adding 50 µl 1N hydrochloric acid.

20 The insulin or glucagon molecule was cleaved into a number of peptide fragments. These were separated and isolated by reverse phase HPLC using a suitable C-18 column (Hibar LiChrosorb RP-18, 5µm particles provided by Merck AG, Darmstadt, FRG). The fragments were eluted with the following solvents:

25 A. 0.2 M sodium sulfate and 0.1 M phosphoric acid, pH 2.5;
B. Acetonitrile/water, 50%;

30 on a linear gradient of from 90% A/10% B to 80% A/20% B for 0-5 min. and subsequently for 50 min. with 80% A/20% B. The isolated fragments were subjected to amino acid sequencing by automated Edman degradation, using an Applied Biosystems (Foster City, CA, USA) Model 470A gas-phase sequencer, and the phenylthiohydantoin (PTH-) amino acids were analyzed by high performance liquid chromatography as described by L. Thim et al., "Secretion of

EXAMPLE 1

A library from *A. aculeatus* consisting of approx. 1.5×10^6 individual clones in 150 pools was constructed.

5

DNA was isolated from 20 individual clones from the library and subjected to analysis for cDNA insertion. The insertion frequency was found to be >90 % and the average insert size was approximately 1400bp.

10

DNA from some of the pools was transformed into yeast, and 50-100 plates containing 200-500 yeast colonies were obtained from each pool. After 3-5 days of growth, the agar plates were replica plated onto several sets of agar plates. One set of 15 plates was then incubated for 2-4 days at 30°C and overlayed with a casein overlayer gel for detection of protease activity. After incubation overnight at 30°C, protease-positive colonies were identified as colonies surrounded by a white halo.

20 Cells from enzyme-positive colonies were spread for single colony isolation on agar, and an enzyme-producing single colony was selected for each of the protease-producing colonies identified.

25 The positive clones were obtained as single colonies, the cDNA inserts were amplified directly from the yeast colony using biotinylated polylinker primers, purified by magnetic beads (Dynabead M-280, Dynal) system and characterized individually by sequencing the 5'-end of each cDNA clone using the chain-30 termination method (Sanger et al., 1977) and the Sequenase system (United States Biochemical). The DNA sequences of two enzyme genes are shown in SEQ ID Nos. 1 and 2, respectively.

Subsequently, the cDNA encoding the protease was isolated for

restriction enzymes HindIII and XbaI which excised the DNA insert. DNA from one of these clones was retransformed into yeast strain JG169.

5 The DNA sequences of several of the positive clones were determined. Two DNA sequences encoding a protease are shown in SEQ ID Nos. 1 and 2, respectively.

EXAMPLE 2

10

In order to express the genes in *Aspergillus*, cDNA is isolated from one or more representatives of each family using the above described procedure by digestion with HindIII/XbaI or other appropriate restriction enzymes, size fractionation on a gel and 15 purification and subsequently ligated to pHD414, resulting in the plasmids pA1P1 and pA1P2. After amplification in *E. coli*, the plasmids are transformed into *A. oryzae* or *A. niger* according to the general procedure described above.

20 **Test of *A. oryzae* transformants**

Each of the transformants was inoculated in the center of a Petri dish with FG-4 agar. After 5 days of incubation at 30°C 4 mm diameter plugs were removed from the center of the colonies 25 by means of a corkscrew. The plugs were embedded in a casein overlayer gel, containing 0.5% casein and 1% agarose in a buffer with a pH of 5.5, and incubated overnight at 40°C. The protease activity was identified as described above. Some of the transformants had halos which were significantly larger than the 30 *Aspergillus oryzae* background. This demonstrates efficient expression of protease in *Aspergillus oryzae*. The 8 transformants with the highest protease activity were selected and inoculated and maintained on YPG-agar.

After 3-4 days of fermentation with sufficient agitation to

30

ensure good aeration, the culture broths were centrifuged for 10 minutes at 2000 g and the supernatants were analyzed.

5 A volume of 15 μ l of each supernatant was applied to 4 mm diameter holes punched out in a casein overlayer gel (25 ml in a 13 cm diameter Petri dish). The protease activity was identified by the formation of a white halo on incubation.

Fed batch fermentation

10 Subsequently, protease I and II, respectively, were produced by fed batch fermentation of *A. oryzae* expressing the enzyme using the procedure described above.

EXAMPLE 3

15

Characterization of Protease I and II

20 The supernatant resulting from the fed batch fermentation above was used for the characterization performed as described in the Materials and Methods section above. Proteolytic activity was measured as HPU/l at pH 5.5 using the above described procedure.

Inhibition tests gave the following results:

25

	% Residual activity			
	EDTA	Pepstatin	PEFABLOC	PMSF
Protease I	104	91	83	92
Protease II	97	9	90	108

30

The inhibition of Protease II by Pepstatin shows that it is an

35 the other hand, shows that it is an acid protease.

pH activity profiles are shown in Fig. 1. It is seen that both enzymes have optimum activity at pH 5, and that Protease I is active in a more narrow range than Protease II. Thus, protease I exhibits more than 60% activity in the range of pH 4-6, 5 whereas Protease II exhibits more than 60% activity in the range of pH 4-7.

By SDS gel analysis the molecular weights of Protease I and II, respectively, were estimated to 23.000 and 37.000 kDa, 10 respectively. From the IEF analysis the pI of both enzymes are estimated to about 4.

Fig. 2 shows the temperature-activity profiles. They are rather similar for the two enzymes, but with slightly different optimum 15 temperatures, 50°C for Protease I and 45°C for Protease II.

Fig. 3 and 4 show the pH-stability. For each pH, the zero-time activities have been set to 100%, and the absolute values obtained are therefore different. Both proteases are stable at 20 pH 4 and 5. At pH 6, Protease I is unstable, while Protease II has a certain stability (40% residual activity after 30 min). Both enzymes are unstable at pH 7.

Fig. 5 and 6 show the temperature-stability. For each 25 temperature, the zero-time activities have been set to 100%, and the absolute values obtained are different. Both proteases are stable up to 50 °C, but unstable at 60 °C.

Based on the results obtained on hydrolysis of insulin and 30 glucagon by Protease I and Protease II it was found that Protease II does not react with insulin, whereas both proteases hydrolyse glucagon. It can be concluded, that Protease I is a rather unspecific protease, while Protease II is more specific.

EXAMPLE 4

Use of a protease of the invention for viscosity reduction

5 Soy flour (prepared from defatted and peeled soy beans) were pelletized at 95°C and grinded afterwards. The soy flour is suspended in deionized water to 15% dry substance. 5 mg protease I enzyme protein per g of dry substance and 5 mg protease II enzyme protein per g of dry substance, respectively, was added 10 to the soy slurry. The slurry was incubated at 40°C and pH 5-6. The viscosity in the slurry was measured after 1, 2 and 24 hours of incubation on a Brookfield LV DV III viscometer using a small sample adaptor with spindle #31 at 250 rpm. The residual viscosities were as follows:

15

	Prot. I	Prot. II
1 hour	73%	47%
2 hours	59%	38%

20 EXAMPLE 5

Use of a protease of the invention for cleaning of contact lenses

25 In the field of contact lens cleaning it is essential to regularly have both an efficient disinfection and cleaning of the contact lens. One of the most effective ways of disinfecting contact lenses is to immerse them into a solution containing 3% H₂O₂ at pH 3.5 for at least 20 minutes. The H₂O₂ is neutralized 30 with e.g. catalase or a platinum disc before inserting the lens into the eye. Unfortunately no commercially interesting protease till date has been shown to have good effect under these harsh conditions, so a cumbersome second step with addition of a protease after H₂O₂-neutralization is needed to remove the

mammal products.

5 Protease I and II, respectively, of the invention have been tested with respect to the ability to remove denatured protein from a contact lens. They have been compared to the presently used serin protease and also to porcine pepsin, although the latter is interesting from a technical perspective rather than a commercial perspective.

10 The experimental protocol was as follows:

Materials: Hen Lysozyme, L-6878 from Sigma
"Rhythmic" contact lens' from Essilor (Type II
lens, high-water, nonionic)
15 Protease I produced as described above
Protease II produced as described above
Porcine pepsin, P-6887 from Sigma
Subtilisin carlsberg, Clear-Lens Pro® (Novo
Nordisk A/S).
20 Standard buffer: 0.05 M Na₂HPO₄, 0.9% NaCl pH 7.5
Reagent buffer: 0.05 M Na₂HPO₄, 0.9% NaCl, 3% H₂O₂, pH
3.5
Scintillation liquid, Optiphase "HiSafe III"
25 Hen lysozyme from Sigma was labelled with ¹⁴C through reductive
methylation and purified.
A solution was made containing 0.05 M Na₂HPO₄, 0.9% NaCl and 0.2
30 mg/ml lysozyme pH 7.5. An amount of ¹⁴C-labelled lysozyme was
added so the CPM (Counts Per Minute) is approximately 200.000.
1.0 ml of the solution was transferred to a scintillation glass.
The contact lens was added and the glass placed in a water-bath
at 35°C for 30 minutes.

was quenched with a sulphuric acid solution and measured in a liquid scintillation counter.

new scintillation glass containing 3 ml of the reagent buffer.

Different amounts of the protease to be tested were added so the final concentrations were 0.1, 0.5, 2.5, 5, 12.5, 50 and 200 µg
5 enzyme protein/ml reagent buffer.

The reaction took place over four hours at 25°C. The quarter lenses were rinsed in 2x3 ml standard buffer. 12 ml scintillation liquid was added and CPM was measured in a Packard
10 2500 TR liquid scintillation counter.

Four lenses were needed to evaluate each protease: Double determinations were made over two days, and a blind reference was needed for each lens.

15 The relative amount of lysozyme removed from the lens during the combined disinfection/cleaning was calculated from the mass balance of each quarter lens. Fig. 7 gives a graphic presentation of the performance of the different proteases.

20 Both proteases are highly suitable for contact lens cleaning purposes. Protease I was found to be very superior to the other proteases. Protease II is very close to porcine pepsin in performance whereas the presently used serin protease shows poor
25 performance. A further advantage of the acidic proteases of the invention is the low activity at the neutral pH found in tear fluid. This lowers the risk of irritation if the lenses are not rinsed properly after disinfection/cleaning.

30 EXAMPLE 6

Use of a protease of the invention for baking

Procedure:

Neutraser® (available from Novo Nordisk A/S). The dough is mixed on a Glutamic 2200 mixer for one minut. It is then placed in a plastic bag and is incubated for 25 min. at 32°C.

5 Thereafter the dough is washed with 2% NaCl (aqueous solution) using the Glutamic mixer in order to remove starch and leave gluten in the dough.

10 The gluten lump is then rolled by hand untill homogeneity and is pressed into the shape of a cylinder which is about 0.5 cm high and 2.5 cm in diameter and has a hole in the center. The gluten lump is pressed into shape for 30 min at 25°C. Subsequently, the gluten cylinder is hung on a hook and a 2 g weight is placed in the hole. Everything is placed under water at 25°C.

15 The stretching of the gluten cylinder is thereafter measured every 15 min untill it breaks.

20 Enzymes are dosed on an Anson Unit basis (AU), initially trying with 7.5 mAU/kg flour, which is the optimal dose for Neutraser®. (In the Anson-Hemoglobin method for the determination of proteolytic activity denatured hemoglobin is digested at a temperature of 25°C, pH 7.5 and a rection time of 10 min. The undigested hemoglobin is precipitated with trichloroacetic acid (TCA) and the amount of TCA soluble product is determined with phenol reagent, which gives a blue colour with tyrosine and tryptophan. 1 AU is the amount of enzyme which digests hemoglobin at an initial rate such that there is liberated per minute an amount of TCA soluble product which gives the same colour with phenol reagent as one milliequivalent of tyrosine).

30 Fig. 8 shows the stretching curves of gluten without enzyme and with Neutraser®, Protease I and Protease II. The curves are means of 6-7 determinations with the same dose of enzyme. As can be

Protease I in a dose of 7.5 mAU/kg flour does not weaken the gluten as much as the same dose of Neutraser®. The gluten cylinder gets longer before it breaks, and the rate of elongation is lower.

5

Addition of 2.3 mAU/kg flour of protease II, which was the largest amount possible in this system, almost weakens the gluten as much as 7.5 mAU/kg of Neutraser®. The gluten breaks a little later, and the shape of the curves are not identical.

10 This shows that protease II is approximately 3 times as efficient on an AU basis as Neutraser® for gluten weakening.

15 In conclusion the proteases of the invention constitutes a desirable alternative to chemicals conventionally used for gluten weakening, a widely used example of which is SMS (sodium metabisulphite).

EXAMPLE 7

20 Use of a protease of the invention for animal feed

Ground defatted feed quality soy was mixed with deionised water under the conditions described below. The hydrolysis was carried out in two steps in order to simulate the pH conditions in the 25 stomach and the small intestine. The performance of Protease II of the invention was compared with that of Bio-Feed Pro, which by Brenes *et al.*, 1993, has been demonstrated to result in improved weight gain and feed efficiency when used in broiler diets.

30

Hydrolysis conditions:

Hydrolysis mixture : 70 g ground defatted soy
230 g deionised water

37

pH : 1st step 4.0
 : 2nd step 6.5
 Time : 1st step 180 minutes
 : 2nd step 180 minutes
 Enzymes : 1st step I) Pepsin 1.92g
 : (Merck art. 7190)
 : II) I + Bio-Feed Pro 3.0L
 : 5.5 AU/kg soya
 : III) I + protease II
 : 0.19 AU/kg soya
 15 2nd step I) Pancreatin 6g
 : (Sigma P 1750)
 : II) I + Bio-Feed Pro 3.0L
 : 5.5 AU/kg soya
 : III) I + Protease II
 : 0.19 AU/kg soya
 20 Bio-Feed Pro® is available from Novo Nordisk A/S. Protease II
 was obtained as described above.
 25 The enzymes were added at start 0 minutes. During the hydrolysis
 °Brix and osmolality were measured to follow the reaction
 course. According to Adler-Nissen (1986) the osmolality values
 can be used for calculation of the Degree of Hydrolysis (DH) by
 the following equation:
 30

$$DH = \frac{\Delta C}{S\% \times f_{osm}} \times \frac{1}{\omega} - \frac{1}{h_{tot}} \times 100\%$$

where Δ is the increase in osmolality mOSM, $S\%$ is protein

H₂O.

$$f_{osm} = \frac{1000}{100 - DM\%} =$$

5

Further the average Molecular Weight was analysed of the sulpho salicylic acid soluble phase of the N-components of the hydrolysis mixture after 90 minutes (1st step) and 0, 15 and 180 minutes (2nd step). The Molecular Weight analyses were performed 10 by the following method:

1. Principle

The sample is diluted, filtrated and injected into a liquid 15 chromatographic system, operating in the Gel Permeation Chromatography (GPC) mode. This separation technique utilizes a liquid flow through a column filled with porous particles having pores with a well-defined pore diameter. When a solution of peptides having different molecular size passes through the 20 column, the small peptides will be able to flow into the pores, while the larger peptides will be excluded from the pores. Thus, the peptides in a solution will be separated according to molecular size (and weight) as the large peptides will be eluted faster from the column than the small peptides. A detector at 25 the column outlet continuously measures the effluent. The chromatographic system is calibrated with peptides with known molecular weight.

2. Chromatographic equipment

30

2.1 HPLC system consisting of

High Pressure pump, WATERS M 510, flow rate 0.7 ml/min.

Injector, Waters WISP M 710

Detector Waters M 440, with wavelength extension to 214 nm.

2.3 Integration/data processing, Waters 820 MAXIMA SIM chromatography data system with 810/820 GPC option.

3. Reagents

5

- 3.1 Phosphate buffer, $\text{NaH}_2\text{PO}_4 \cdot 2\text{H}_2\text{O}$
- 3.2 Ammoniumchloride, NH_4CL
- 3.3 Trifluoroacetic acid (TFA), CF_3COOH
- 3.4 Acetonitrile, CH_3CN

10

3.5 Mobile phase:

0.05 M Phosphate buffer / 0.5 M Ammoniumchloride solution containing 0.1% TFA and 25% Acetonitrile

15 4. Description

4.1 Calibration

The chromatographic system is calibrated by means of injections of numerous peptide standards with known molecular weight. The 20 molecular weight of each standard is plotted semilogarithmic versus the observed volume of mobile phase needed to elute the peptide from the column. By a least squares calculation the best fitting 3rd order polynomium is calculated. This curve represents the calibration curve.

25

4.2 Analysis

The sample is diluted/dissolved in mobile phase to approx. 5 mg/ml. The solution is filtered through a 22 μm filter and 20 μl is used for injection into the chromatograph. The detector 30 response versus elution volume is recorded. The recorded curve - the chromatogram - shows the actual molecular weight distribution of the sample. To allow for calculations as to accumulated weight distribution and average molecular weight calculations the chromatogram is divided into small time (and

5. Calculation

Results are given in terms of weight and number average molecular weights.

$$5 \quad \bar{M}_w = \frac{\sum_i (A_i * M_{w,i})}{\sum_i A_i}, \quad \bar{M}_n = \frac{\sum_i A_i}{\sum_i (A_i/M_{w,i})}, \quad \text{where}$$

10

\bar{M}_w : Weight average molecular weight

15

\bar{M}_n : Number average molecular weight

A_i : Area of chromatogram for each segment, measured as the accumulated detector response over each time interval.

20

$M_{w,i}$: The corresponding molecular weight for each segment. The value is calculated by means of the calibration curve using the average elution volume over the time interval.

25

RESULTS

The values for °Brix, mOSM and %DH are given in the table below:

HYDROLYSIS OF FEED SOY WITH PEPSIN, BIO-FEED PRO, PROTEASE II AND PANCREATIN

TER: °BRIX							
	STEP I, MIN.						
	0	5	10	15	30	45	60
P	5.09	6.135	6.505	6.625	6.9275	7.345	7.745
P	5.09	6.125	6.325	6.545	7.245	7.465	7.565
E II	5.09	6.505	6.845	7.105	7.825	8.405	8.605

TER: °BRIX							
	STEP II, MIN.						
	180	185	190	195	210	225	240
P	12.965	15.135	15.4025	15.637	16.135	16.415	16.705
P	12.965	15.165	15.165	15.725	16.105	16.4	16.525
E II	13.605	15.605	15.925	16.025	16.365	16.685	16.885

TER: mOSM		STEP I, MIN.									
		0	5	10	15	30	45	60	90	120	180
	347	362	362	360.5	363.5	366	368	370.5	373	381.5	
PRO	347	365	364	366	367	371	373	379	380	385	
E II	347	371	382	391	411	421	427	439	447	463	

TER: mOSM		STEP II, MIN.									
		180	185	190	195	210	225	240	270	300	360
	468	996	1009	1015.5	1037.5	1054.5	1068.5	1087.5	1111	1148	
PRO	468	1013	1017	1033	1048	1058	1069	1094	1113	1145	
E II	548	1118	1127	1135	1152	1161	1176	1201	1227	1284	

TER: mOSM INCREASE STEP I, MIN.									
	0	5	10	15	30	45	60	90	120
PRO	0	15	15	13.5	16.5	19	21	23.5	26
II	0	24	35	44	64	74	80	92	100
									116

TER: mOSM INCREASE STEP II, MIN.									
	180	185	190	195	210	225	240	270	300
PRO	0	528	541	547.5	569.5	586.5	600.5	619.5	643
II	0	545	549	565	578	590	601	626	645
		570	579	587	604	613	628	653	679
									736

TER: % DH		STEP I, MIN.									
		0	5	10	15	30	45	60	90	120	180
	0	2.86	2.86	2.57	3.14	3.62	4.00	4.47	4.95	6.57	
PRO	0	3.43	3.24	3.62	3.81	4.57	4.95	6.09	6.28	7.24	
E II	0	4.57	6.66	8.38	12.19	14.09	15.23	17.52	19.04	22.09	

The results of the molecular weight analysis is given below:

5		Step I 90 min	Step II		
			0 min	15 min	180 min
	Pepsin	960	1070	680	520
	Bio-Feed Pro	880	1020	690	510
	Protease II	650	630	530	480

10 The apparent Molecular Weight is increased when pH is adjusted to 6.5 as undigested soy protein is more soluble at pH 6.5 than at pH 4.0.

15 It is seen that protease II releases more protein and peptides and degrade the proteins more than Bio-Feed Pro, it therefore concluded that protease II is superior to Bio-Feed Pro.

20 Since protease II of the invention has optimum activity in acid pH range, this enzyme will therefore perform already in the stomach of the animal, thus an overall improvement on feed efficiency should be achieved compared to Bio-Feed Pro when applied in feed for young animals. The above results supports this conclusion.

SEQUENCE LISTING

5 (1) GENERAL INFORMATION:

- (i) APPLICANT:
 - (A) NAME: NOVO NORDISK A/S
 - (B) STREET: Novo Alle
 - (C) CITY: Bagsvaerd
 - (D) COUNTRY: DENMARK
 - (F) POSTAL CODE (ZIP): DK-2880
 - (G) TELEPHONE: +45 44448888
 - (H) TELEFAX: +45 4449 3256
 - (I) TELEX: 37304
- (ii) TITLE OF INVENTION: *Aspergillus aculeatus* protease
- (iii) NUMBER OF SEQUENCES: 2
- (iv) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

20 (2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1124 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Aspergillus aculeatus*

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

AATTAAGCAT CCTCCATCTT CAAAGCTCAA TCTCGCTAAC TCCCGCTCTT CTCTCGATCT	60
CATCATCCCA ATAACCTCGGA CACAATGAAG ACCTCTGCTC TCTTGACCGC TGGCCTGTTG	120
GCCACCGCTG CTATTGCTGC TCCTCTCACC GAGAAGCGCG CAGCTGCTCG CGCTGCCAAG	180
CGTGGCACCA GCGCAAGAG CAACCCCCCT CTCAAGCCCCG GCACCCAGCGA GGGCATCAAC	240
CTGACCGGCT CCAAGAACAC CGAGTACTCG TCCAACCTGGG CCGGGCGCGT GCTCATCGGC	300
ACCGGCTACA CTGCCGTAC CGCCGAGTTC ACCATTCCA CCCCCCTCTCT CCCCTCCGGT	360

47

GCCGGCGACG TTGTCAAGGT CACCGTCGAC GCCACCAGCA AGACCGCCGG TACCGCCACC 600
 GTCGAGAACG TCACCAAGGG CACCACCGTC ACCCACACCT TCAGCGGTGG TGGTGATGGT 660
 5 GATCTCTGCG AGTACAAACCG CGAGTGGATC GTCGAGGACT TCGAGGAGAA CTCCCTCCCTC 720
 GTCCCCTTCG CCGACTTCGG CACCGTCACC TTCTCCAGCG CCTACGCCAC CAAGAGCGGC 780
 TCCACCGTTG GTCCCTCCGG CGCCACCATC ATCGACATCG AGCAGAACAA CAAGGTTCTC 840
 10 ACCTCCGTCT CGACCTCCAG CAGCTCCGTC ACCGTCGAGT ATGTTTGAAG GGGACTCCTG 900
 GGGATGTGAA GCGAGAAATGC GGCTTGGGTG GTTGGAGGTC CTTTGGGACG TCGAACGCCT 960
 15 AGGATTCAAC GGGATGAGAT CATTGAAAT GAAGACGAGA ATGAGCGAAT ACTGTCACTG 1020
 ATTGAGATTG TGCTTTGTTG ATTGTGTTAG GGGCTTGCCT CTGAAATTG ACCTTAGTGT 1080
 20 TGCTGCAATA TGATTGCTGT GGTTGAGAAA AAAAAAAA AAAAA 1124
 (2) INFORMATION FOR SEQ ID NO: 2:
 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1425 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 30 (ii) MOLECULE TYPE: cDNA
 35 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 40 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Aspergillus aculeatus
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 45 CTGCTTCTCC TTCTCTTCCT CCTCGTGATA TCTGCTTGAA CATCTCCTCA TCATGGTCGT 600
 CCTCAACAAG GCTGCAGCCC TTCTTCTGGG TCTGACCACC GCGGCCACTG CGGCTCCCTC 120
 50 GGGCGAGAAC CAGGCTTCTG TCCCGGTCAA GAACTTCTCC GTCAAGCAGG TCGAGAACAGGA 180
 GGGCAGCAAG GGACGTACCG TAAACCTGCC GGGTCTGTAT GCGAATGCGC TGGCCAAGTA 240
 TGGCGCCCAAG GTGCCGCCA GCGTCAAGGC CGCCGCCGTC AGTGGCAGCG TCGTGACCAC 300
 55 CCCGCAGGCC AACGACGTCT CCTACCTGAC CCCCCTCACC GTGGCAGCT CGACCTTGAA 360
 CCTGGACTTC GACACGGAT CGCCGATCT CTGGGTCTTC TCCTCGGAGC TGGCCGCCCTC 420
 60 CTCGCGCACC GGCCACAGCA TCTACACCCCC CGGCAGCACC GCCCAGAACG TGTCCGGCTA 480
 CAGCTGGAGC ATCTCCTACG GCGACGGCAG CTCCGCCAGC GCGCAGCTCT ACAAGGACAA 540
 GGTCACCGTC GGCACGGTGA CGGCCAGCAG CCAGGCCGTC GAGGCCGCCA CGCCGATCAG 600
 GGCCGCCCTC GTCCTCGGCT CGCCGCCCTC CGCTCTGCCCT CGCTCTGCCCT TGGCCGCCCT 660
 CATCGACTCC TCCAAGTACA CGGCGTCCCT GAGCTACGCC AACGTCGAGG AGTCGACAGG 840

48

	CTTCTGGCAA	TTCACCGCCA	GCGGCTACAG	CGTGGGCTCG	GCCTCCCACT	CCTCCTCTTT	900
	CTCCGCCATT	GATGACACCG	GCACCCACCCCT	CATCCTCCCTC	GACGACTCCA	TCGTCTCCAC	960
5	CTACTACAAG	AGCGTCAGCG	GCGCCTCCTA	CAGCTACAAAC	TACGGCGGCT	ACGTCTTCTC	1020
	CTGCTCCGCC	AGCCTGTCCA	ACTTCAGCGT	CAAGATCGGC	TCCTACACCG	CCGTCTGTCCC	1080
	CGGCAAGTAC	ATCAACTACG	CCCCCATCTC	CACCGGCAGC	TCCACCTGCT	ACGGCGGCAT	1140
10	CCAGTCCAAC	GAGGGCCTCG	GTCTGTCCAT	CCTGGGTGAT	GTCTTCCTCA	AGAGCCAGCA	1200
	CGTGGTCTTT	GACTCGCAGG	GTCCGAGAAT	CGGGTTGCC	GCGCAGGCCT	AGATCGTTG	1260
15	ATTGGGTTG	TGGATGTGGG	TGATGCTTGG	TGGTGGTCTG	AGTCGTGGTC	TATGTGGGCG	1320
	TGAATATACT	ACTGTATATA	GTACTGTACA	TACCGGGGTG	GTGAACATAT	GGTCTGGTCA	1380
20	ATGAATATAT	GTCTTGATG	TTATGCTTCT	GTGGAAAAAA	AAAAAA		1425

25

REFERENCES

Aviv, H. & Leder, P. 1972. Proc. Natl. Acad. Sci. U. S. A. 69: 1408-1412.

Becker, D. M. & Guarante, L. 1991. Methods Enzymol. 194: 182-187.

Chirgwin, J. M., Przybyla, A. E., MacDonald, R. J. & Rutter, W. J. 1979. Biochemistry 18: 5294-5299.

Gubler, U. & Hoffman, B. J. 1983. Gene 25: 263-269.

Sambrook, J., Fritsch, E. F. & Maniatis, T. 1989. Molecular Cloning: A Laboratory Manual. Cold Spring Harbor Lab., Cold Spring Harbor, NY.

Sanger, F., Nicklen, S. & Coulson, A. R. 1977. Proc. Natl. Acad. Sci. U. S. A. 74: 5463-5467.

Brenes, A. et al., Poultry Science, 72, 2281-2293, 1993.

Adler-Nissen, J. Enzymic Hydrolysis of Food Proteins, Elsevier Applied Science Publishers London and New York, 1986.

Takahashi, K. et al., 1991, The Primary Structure of *Aspergillus niger* Acid Proteinase A*, The Journal of Biol. Chemistry, Vol. 266, No. 29, pp. 19480-19483.

Choi, G.H. et al., Molecular analysis and overexpression of the gene encoding endothiapepsin, an aspartic protease from *Cryptosporidium parvum*. 1993. Gene 125:125-131.

50

Acid Protease-encoding Gene (*pepA*) from *Aspergillus oryzae*,
Biosci. Biotech. Biochem., 57(7):1095-1100.

Inoue, H. et al., 1991, The Gene and Deduced Protein Sequences
5 of the Zymogen of *Aspergillus niger* Acid Proteinase A*, The
Journal of Biological Chemistry, Vol. 266, No. 29, pp. 19484-
19489.

Berka, R.M. et al., 1993, Isolation and characterization of the
10 *Aspergillus oryzae* gene encoding aspergillopepsin O, Gene,
125:195-198.

Berka, R.M. et al., 1990, Molecular cloning and deletion of the
gene encoding aspergillopepsin A from *Aspergillus awamori*, Gene
15 86:153-162.

Berka, R.M. et al., 1990, Corrigendum, Molecular cloning and
deletion of the gene encoding aspergillopepsin A from
Aspergillus awamori, Gene 96:313.

20

CLAIMS

1. A DNA construct comprising a DNA sequence encoding an enzyme exhibiting protease activity, which DNA sequence comprises
5 the DNA sequence shown in SEQ ID No. 1 or an analogous sequence thereof being at least 80% homologous to the DNA sequence shown in SEQ ID No. 1.
2. A DNA construct comprising a DNA sequence encoding an enzyme exhibiting protease activity, which DNA sequence comprises
10 the DNA sequence shown in SEQ ID No. 2 or an analogous sequence thereof being at least 80% homologous to the DNA sequence shown in SEQ ID No. 2.
- 15 3. The DNA construct according to claim 1 or 2, in which the DNA sequence encoding an enzyme exhibiting proteolytic activity is obtainable from a microorganism.
4. The DNA construct according to claim 3, in which the DNA
20 sequence is obtainable from a filamentous fungus or a yeast.
5. The DNA construct according to claim 4, in which the DNA sequence is obtainable from a strain of *Aspergillus*, *Rhizopus*,
25 *Trichoderma*, *Penicillium*, *Fusarium*, *Schytalidium* or *Humicola*.
6. The DNA construct according to claim 5, in which the DNA sequence is obtainable from a strain of *Aspergillus*, in particular a strain of *Aspergillus aculeatus*, *Aspergillus niger* or *Aspergillus oryzae*.
- 30 7. The DNA construct according to claim 6, in which the DNA sequence is isolated from or produced on the basis of a DNA library of *Aspergillus aculeatus*, CBS 101.43.

9. A cell comprising a DNA construct according to any of claims 1-7 or a recombinant expression vector according to claim 8.

10. A cell according to claim 9, which is a eukaryotic cell, in particular a fungal cell, such as a yeast cell or a filamentous fungal cell.

11. A cell according to claim 10, wherein the cell belongs to a strain of *Aspergillus*, in particular a strain of *Aspergillus niger* or *Aspergillus oryzae*.

12. A method of producing an enzyme exhibiting proteolytic activity, the method comprising culturing a cell according to any of claims 9-11 under conditions permitting the production of the enzyme, and recovering the enzyme from the culture.

13. An enzyme exhibiting proteolytic activity, which enzyme is encoded by a DNA construct according to any of claims 1-7 or produced by the method according to claim 12.

14. An enzyme with protease activity, which enzyme is active at a pH below 7 and in the presence of up to 5% hydrogen peroxide.

15. An enzyme with protease activity, which enzyme preferably hydrolyses Phe-Val or Lys-Tyr linkages in bovine glucagon.

16. An enzyme according to any of claims 13-15, which is immunologically reactive with an antibody raised against a purified protease derived from *Aspergillus aculeatus*, CBS 101.43 and being encoding by the DNA sequence shown in SEQ ID No. 1 or 2.

17. An enzyme according to any of claim 13-17 which is

bacterium or a fungus.

19. An enzyme according to claim 18, which is obtainable from a strain of *Aspergillus*, *Rhizopus*, *Trichoderma*, *Penicillium*, 5 *Fusarium*, *Schytalidium* or *Humicola*.

20. An enzyme according to claim 19, which is obtainable from a strain of *Aspergillus aculeatus*.

10 21. An enzyme preparation useful for the degradation of plant cell wall components, said preparation being enriched in an enzyme exhibiting protease activity according to any of claims 13-20.

15 22. The preparation according to claim 21, which additionally comprises one or more other plant cell wall degrading enzymes such as a pectin lyase, pectate lyase, endoglucanase, arabinanase, xylanase, glucanase, galactanase, mannanase, α -galactosidase, rhamnogalacturonase, pectin acetyl esterase, 20 polygalacturonase, protease, exo-peptidase or pectin methylesterase.

25 23. Use of an enzyme according to any of claims 13-20 or an enzyme preparation according to claim 21 or 22 for the degradation or modification of protein containing substances.

20 24. Use of an enzyme according to any of claims 13-20 or an enzyme preparation according to claim 21 or 22 for cleaning of contact lenses.

30 25. Use of an enzyme according to any of claims 13-20 or an enzyme preparation according to claim 21 or 22 for the preparation of baked products.

1/8

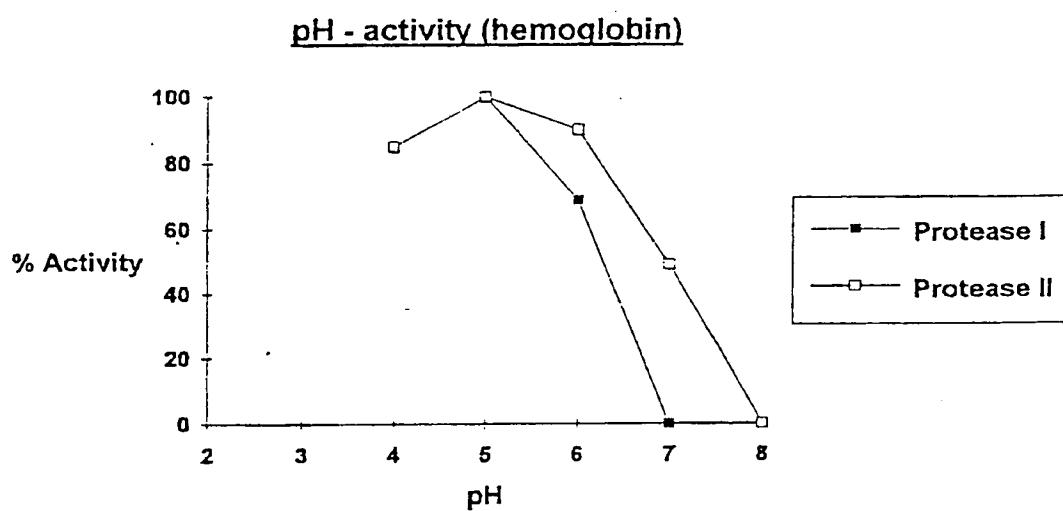


Fig. 1

2/8

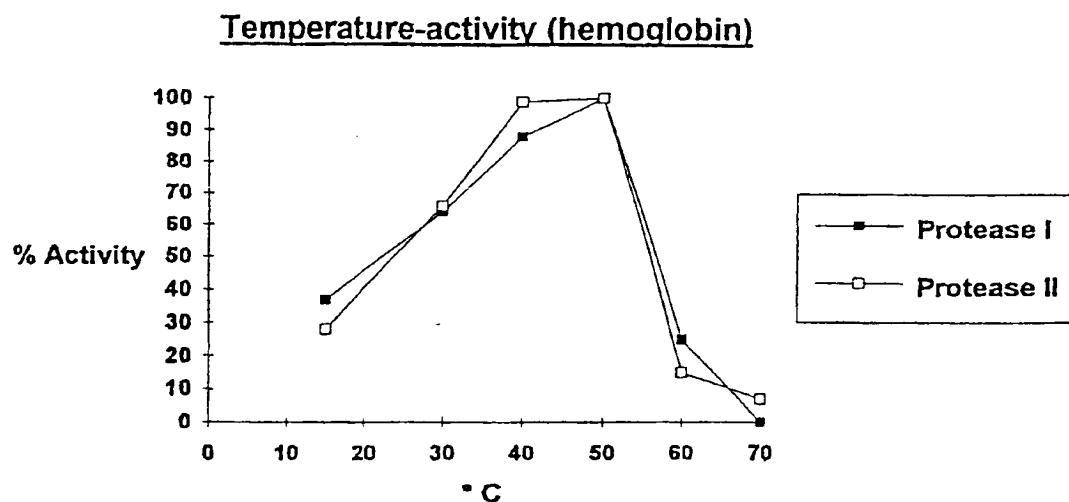


Fig. 2

3/8

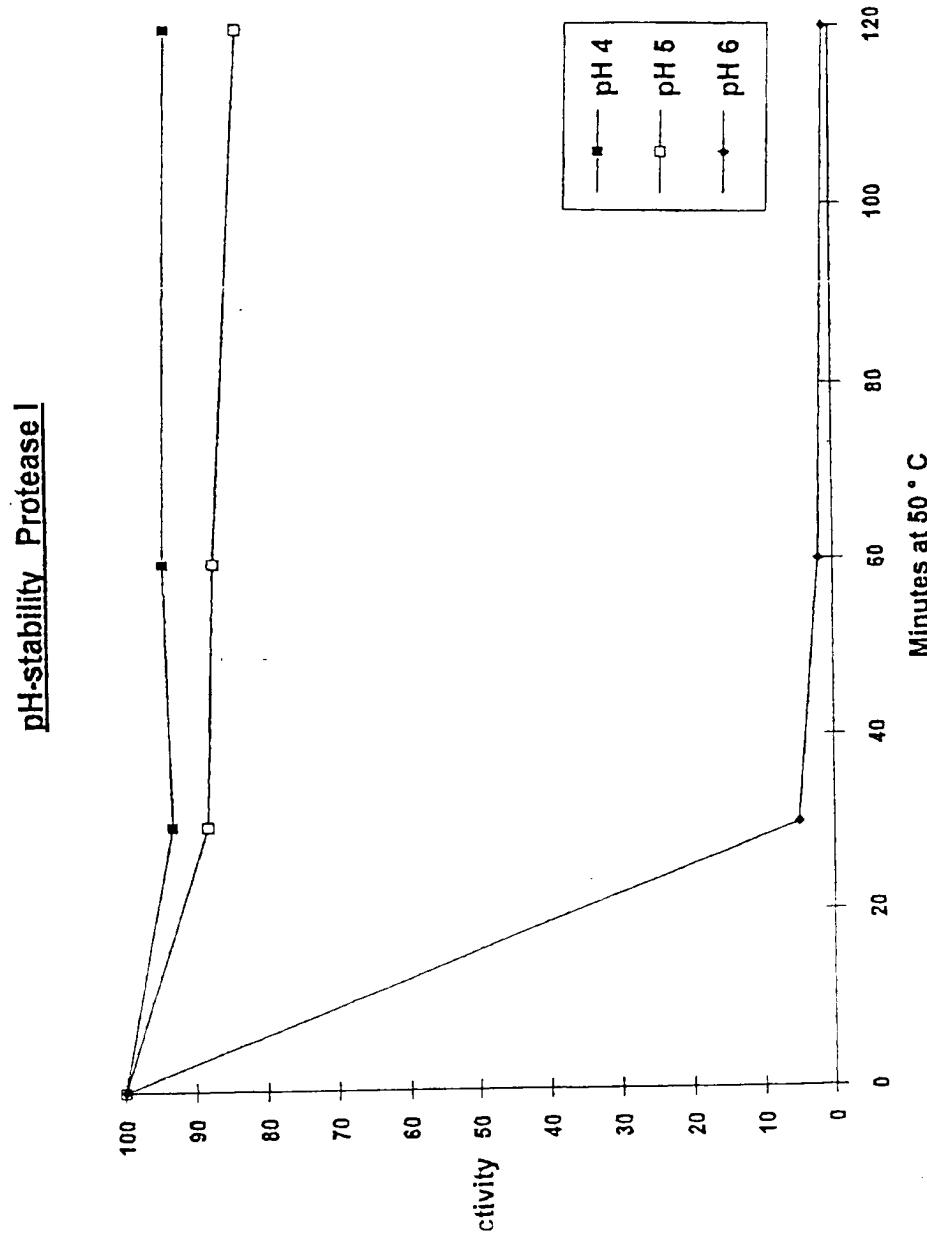


Fig. 3

4/8

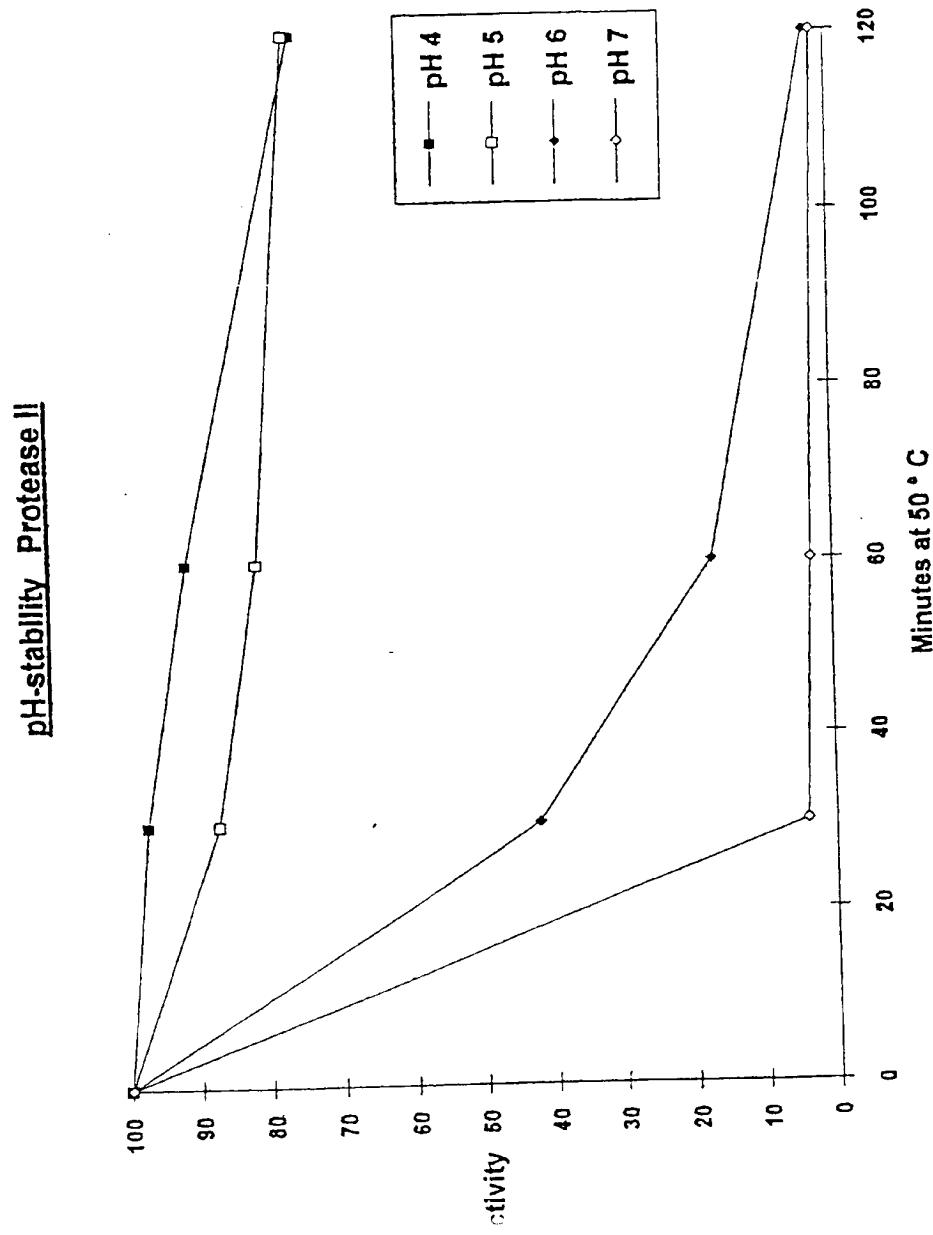


Fig. 4

5/8

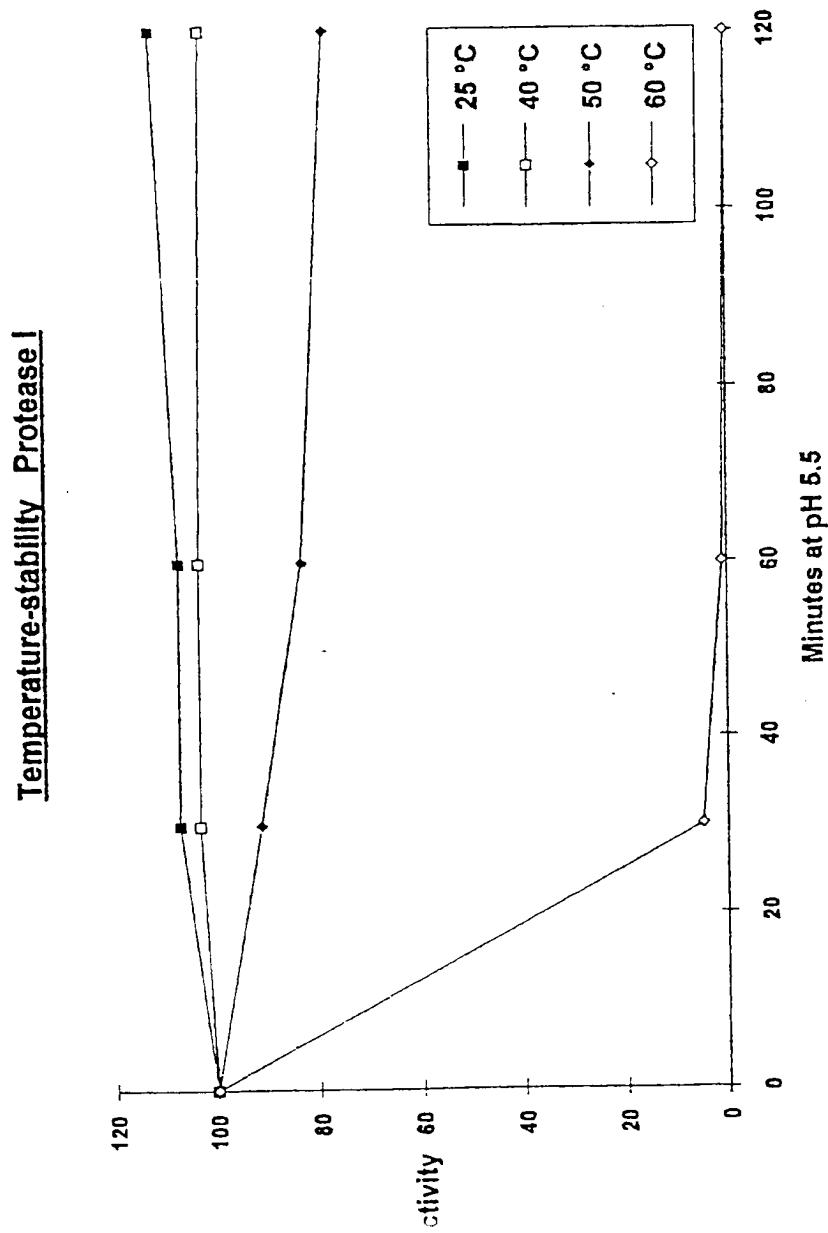


Fig. 5

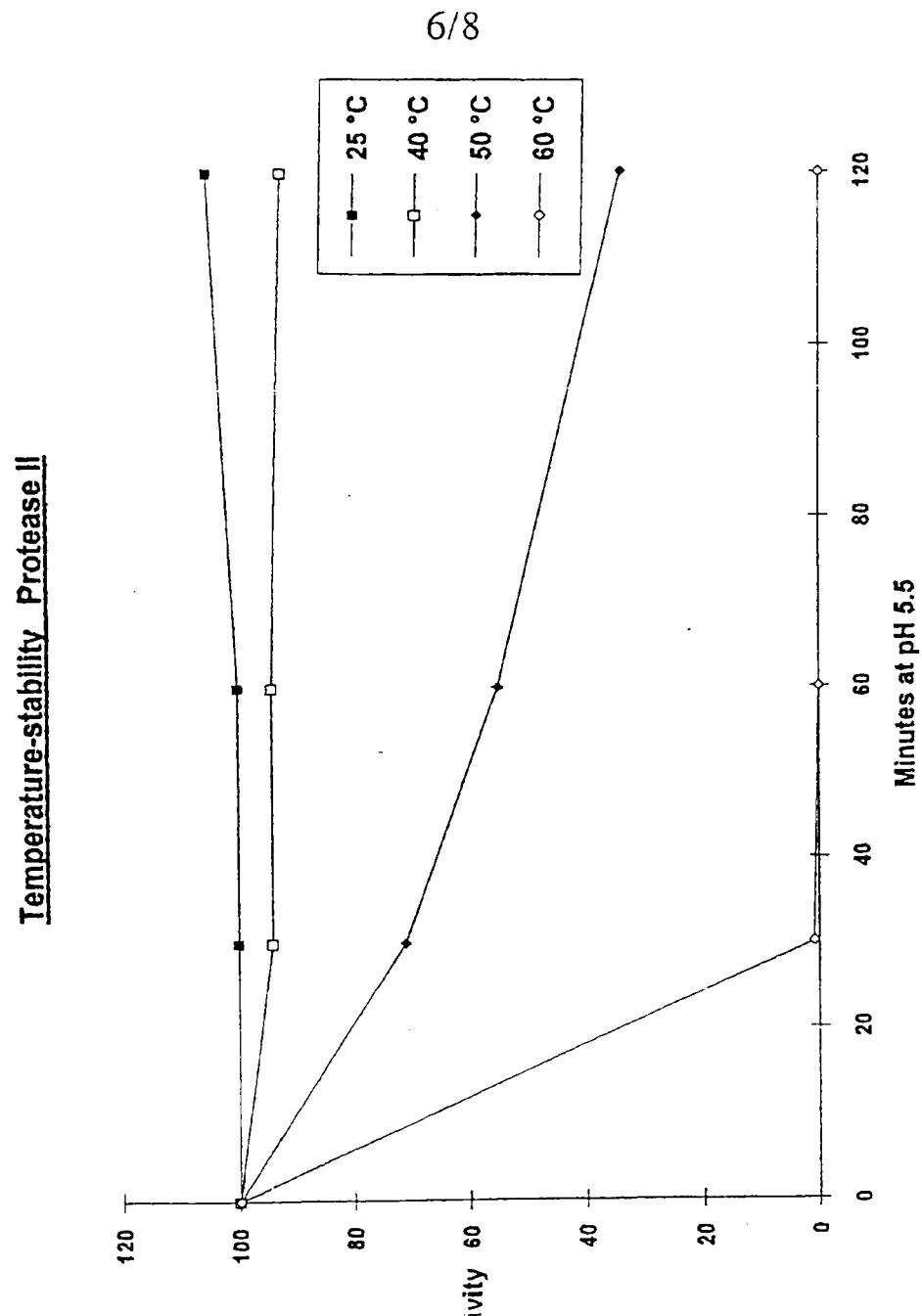


Fig. 6

7/8

Protease performance in 3% H₂O₂ pH 3.5

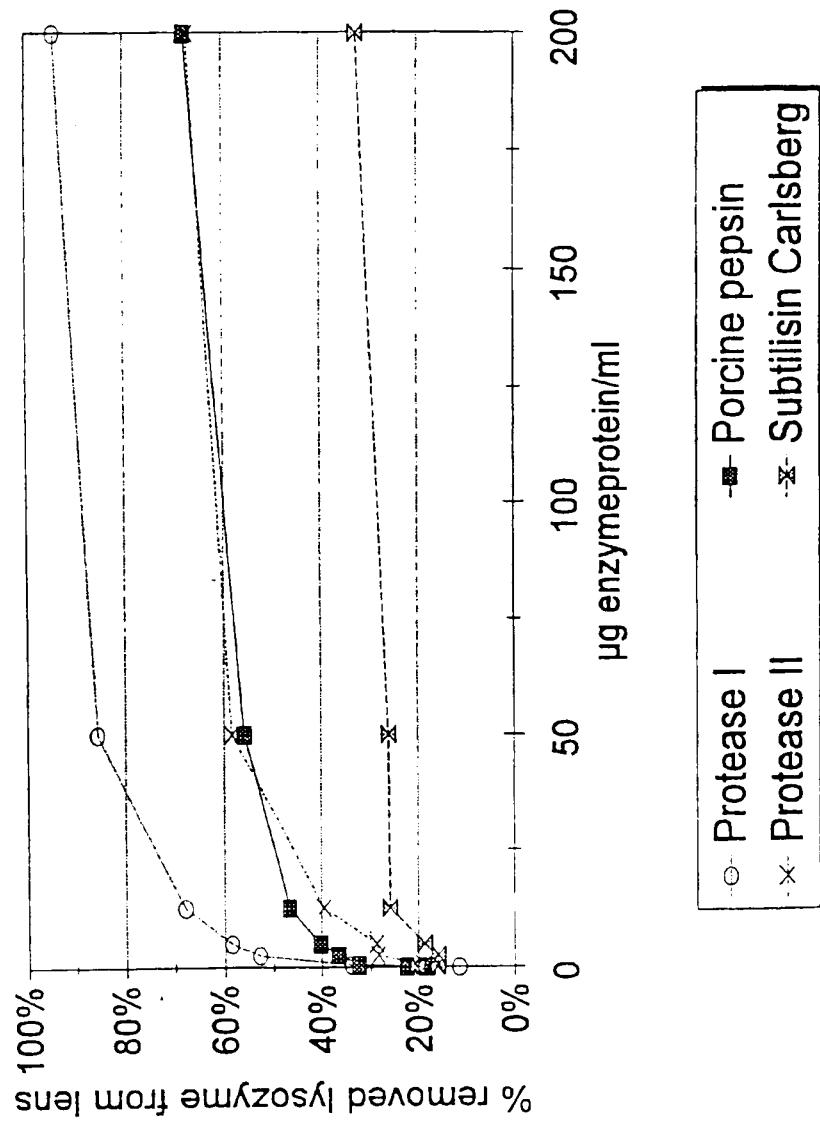


Fig. 7

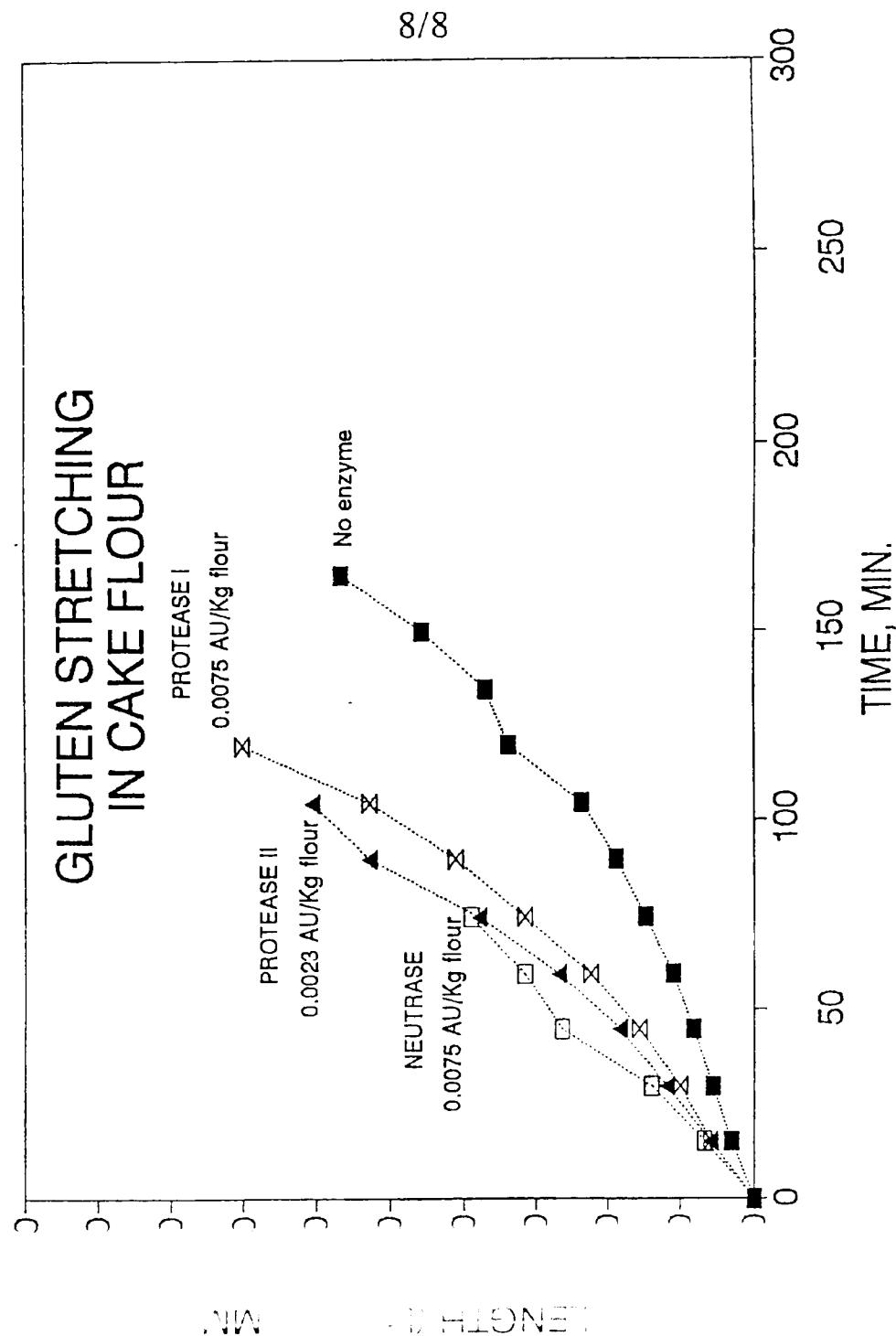


Fig. 8

INTERNATIONAL SEARCH REPORT

International application No.

PCT/DK 94/00274

A. CLASSIFICATION OF SUBJECT MATTER

IPC5: C12N 9/62

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC5: C12N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

SE,DK,FI,NO classes as above

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

MEDLINE, BIOSIS, WPI, IFIPAT

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	US, A, 3492204 (YOSHIHISA KOAZE ET AL), 27 January 1970 (27.01.70) --	1-13,16-26
X	US, A, 3509024 (JÖRG H. JÜRGENS ET AL), 28 April 1970 (28.04.70) --	1-13
X	THE JOURNAL OF BIOLOGICAL CHEMISTRY, Volume 266, No 29, October 1991, Kenji Takahashi et al, "The Primary Structure of Aspergillus niger Acid Proteinase A", page 19480 --	1,3-13,16-26

 Further documents are listed in the continuation of Box C. See patent family annex.

* Special categories of cited documents:	
A document defining the general state of the art which is not considered to be of particular relevance	*T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
E earlier document but published on or after the international filing date	*X* document of particular relevance: the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*Y* document of particular relevance: the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
O document referring to an oral disclosure, use, exhibition or other means	*&* document member of the same patent family
P document published prior to the international filing date but later than the priority date claimed	

*None of the cited documents is of the international application.

Name and mailing address of the inventor:
Swedish Patent Office
Box 5055, S-102 42 STOCKHOLM
Facsimile No. + 46 8 666 02 86

Other name of inventor:
Carolina Gomez Lagerlöf
Telephone No. + 46 8 732 25 00

Form PCT/ISA 210 (second sheet) (July 1997)

INTERNATIONAL SEARCH REPORT

International application No.

PCT/DK 94/00274

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	GENE, Volume 125, 1993, Randy M. Berka et al, "Isolation and characterization of the <i>Aspergillus oryzae</i> gene encoding aspergillopepsin O" page 195 -- -----	2

INTERNATIONAL SEARCH REPORT

International application No.

PCT/DK 94/00274

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:

2. Claims Nos.: because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. Claims Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see next sheet

1. As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:



No protest accompanied the payment of additional search fees.

Form PCT/ISA/210 (continuation of first sheet (1)) (July 1992)

INTERNATIONAL SEARCH REPORT

International application No.

1. A DNA sequence shown in SEQ ID No. 1 according to claim 1. The sequence SEQ ID No. 1 encodes an enzyme exhibiting protease activity, called protease 1.
2. A DNA sequence shown in SEQ ID No. 2 according to claim 2. The sequence SEQ ID No. 2 encodes an enzyme exhibiting protease activity, called protease 2.

The technical relationship between the two enzymes, apart from the protease activity, has not been made clear. See PCT Rule 13.2.

INTERNATIONAL SEARCH REPORT
Information on patent family members

01/10/94

International application No.
PCT/DK 94/00274

Patent document cited in search report	Publication date	Patent family member(s)		Publication date
US-A- 3492204	27/01/70	NONE		
US-A- 3509024	28/04/70	CH-A- 525251	15/07/72	
		DE-A,B,C 1617279	18/02/71	
		FR-M- 6225	05/08/68	
		GB-A- 1150293	30/04/69	
		NL-A- 6612046	28/02/67	

Form PCT/ISA.2/10 (patent family annex) (15.9.1992)